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qq	252(O AATTCTTTCAAATTTTAGCTAAAAGTCTTGTAATAACTAAAGAATAATACACAATCTCGA 2579
Qy	2581	gaaaaaaaacacataataaatttgaatttcgaccgcggtacccggaattcgagct 264
QO	2580	CACGGAAAAAAAACACATAATAAATTTGAATTTCGACCGCGGTACCCGGAATTCGAGGT 263
Qy	2641	cggtacccgggggatcttcccgatctagtaacatagatgacaccgcgcgcg
qa	2640	CGGTACCCGGGGATCTTCCCGATCTAGTAACATGATGACACCGCGCGCG
oy g	70	ctagtttgcgcgctatattttgttttctatcgcgtattaaatgtataattgcgggactct 27
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QQ	2880	
Qy	2941	agtttgaagaaaatttattacacactttatgtaaagctgaaa 300
qa	2940	TGAAATTGACCGATCAGAGTTTGAAGAAAATTTATTACACACTTTATGTAAAGCTGAAA 299
δy	00	aaaacggcctccgcaggaagccgttttttcgttatctgatttttgtaaaggtctgataa 3060
qa	3000	GGCCTCCGCAGGAAGCCGTTTTTTCGTTATCTGATTTTTGTAAAGGTCTGATAA 305
QY	3061	tegettgagtaaagaateeggtetgaatttetg 312
QΩ	3060	GTCCGTTGTTTTGTAAATCAGCCAGTCGCTTGAGTAAAGAATCCGGTCTGAATTTCTG 311
Qy	3121	gcttcacgccatgttcgtccgcttttgcccgggagt 318
qq	3120	CTGATGTATAGTTAATATCCGCTTCACCCATGTTCGTCCGCTTTTGCCCGGGAGT 317
QY	3181	cottocotgittgagaagatgtotoogoogatgetttooooggagogacgtotgca 32
QQ	3180	GCCTTCCCTGTTTGAGAAGATGTCTCCGCCGATGCTTTTCCCCGGAGCGACGTCTGA 323
QY	3241	cottttgatgccaccagccgagggcttgtgcttctgattttgtaatgtaatt
qa	3240	GGTTCCCTTTTGATGCCACCAGCCGAGGCTTGTGTCTTCTGTATTGTATGTA
δy	3301	tagottatgatatgtotgaagataatoogcaacooogtoaaacgtgttgataaco 336
qa	3300	AGGTAGCTTATGATATGTCTGAAGATAATCCGCAACCCCGTCAAACGTGTTGATAACC 33
Οy	3361	taatttetttaagtaaaaaetttgatttgagtgatgatgttgtact 342
qq	3360	GTACCATGGTAGCTAATTTCTTTAAGTAAAAACTTTGATTTGAGTGATGATGTGTGTACTT 341
Qy	3421	caccacaagggcatatatagagcacaagacatacacaacaacttgcaaaa 348
qa	3420	IACACTIGCACCACAAGGGCATATATAGAGCACAAGACATACACAACAACAACAACAAA 347
δ	3481	aggaaaatggggagtagcaggctaatctgagggtaac 35
QΩ	3480	TAACTTTGTTGGAGCATTTCGAGG
Qy	3541	aaacatggacttagtgtgaggaaaaagtaco
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Οy	09	a -
qq	3600	rtttgtctcaccctgatttcagttatggaaattacattatgaagctgtgctagag

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Oy 4741 gaatgtatattatatgcataatt Db 4740 GAATGTATATTATATGCATAATT OY 4801 ataatctatgtatatggttagaa	RESULT 4 A60112 5560 bp LOCUS DEFINITION Sequence 5 from Paten ACCESSION A60112 GI:3715128 KEYWORDS SOURCE Transformation vector ORGANISM Transformation vector ATTILE Genetic transformatio AUTHORS TITLE Genetic transformatio TITLE Genetic transformatio TITLE Genetic transformatio De, B.M. PATHORS De, B.M. TITLE Genetic transformatio TITLE Genetic transformatio Patent: WO 970569-A PLANT GENETIC SYSTEMS	FEATURES Location/Qua source 1.5560 / Organism="T / Ab_xref="ta BASE COUNT 1533 a 1199 c ORIGIN Query Match 40.7%; Best Local Similarity 93.5%; Matches 2597; Conservative	Qy 1 aattacaacggtatatatcctgc	181 168 241 228	Oy 301 agrceologygactcctagacc Db 288 AGCTCATCGGGGGATCCTAG-AC Oy 361 ggggcggtaccggcaggctgaag Db 347 GGGGGGTACCGGCAGCTGAAG Oy 421 gcttgaagccggccgccgcagc Db 407 GCTTGAAGCCGGCCCCCGCAGGCCGAGGCTGAAG
3661 gatgtttattctagtccagccacccacttatgcaagtctgcttttagcttgattcaaaa 3720 3660 GATGTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	3841 gtcaattgtccttcttgtttggcactattcaatctgttaatgcaattatccagtta 3900 1111111111111111111111111111111111	4081 acagattgttacatggaaaacaaaagtcctctgatagaagtcgcaagtatcacaattt 4140	ttattttttg ttattttttg TTATTTTTTG atttaattat ATTTAATTATA aatgtttatg	aaaatgtgaatttettaatetgtgtgaaacaaccaaaaateaettattgtggaecgga 4	4561 acctaaaacagcatatggtagtttctagggaatctaaatcactaaattaataaaagaa 4620
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4859 4860 180 agtcaggtattatagtccaagcaaaaacataaatttatt 240 agtccagctgccagaaacccacgtcatgccagttcccgt 420 goatgccgcggggggcatatccgagcgctcgtgcatgc 480 gcccgatgacagcgaccacgctcttgaagccctgtgcct 540 227 Gaps 9 GILLIII GCCAGT------ACTCGGCCGTCGAGTACATG 47 06-MAR-1998 yccagtactcggccgtcgaactcggccgtcgagtacatg Length 5560; 2; Indels 179; Transformation vector pTHW142" taxon:126817" 1244 g 1576 t 8 others ion using a PARP inhibitor A 5 20-FEB-1997; MS NV (BE) ualifiers PAT DB 9; Score 2386.8; Pred. No. 0; 0; Mismatches DNA DNA DNA DNA or pTHW142. or pTHW142 vectors

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1515 1666 1575 1726 1635 1786 1695 1846 1755 1906 1815 1875 1547 ATATATATTTTTTCATTTAAAAGCAAAATTTGCCTTTTACTAGAATTATAAATATAGAA 1606 1966 2026 1935 2086 1995 2146 2055 2206 2115 2266 2175 2235 2295 2446 2355 2415 2475 2326 2386 2506 2566 2686 aaaaaaaacttctcaagtctccatcttcctttatgaacattgaaaactatacacaaaaca agicagataaaictiticigggccigicticccaaccicciacaicacticcciategg taacaaccatatatgttgcgattgatctgcaaaaatactgctagagtaatgaaaaatata 1456 1607 1516 1667 1696 1847 1756 1816 1961 1876 2027 2087 2147 2116 2356 1936 1996 2056 2207 2267 2176 2387 2507 2327 2236 2296 2447 2416 2567 g οý g qq q QC δý ٥y ŏ Ωý g Db Db g qq οy δ δ ò ò qq Qγ q δ q δ Q Q Ω δý QΩ Ω qq δ Ob ŏ g

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	2687 TAGCTAAAAGTCTTGTAATAACTAAAGAATAATACACAATCTCGACCACGGAAAAAAAC 27.	VY 2390 acaidadearilyaari 2013 	DNA	Sequence 5 Irom patent AR098311 AR098311.1 GI:1280756	ORGANISM	AUTHORS De Block, M. TITLE Genetic transformation using a PARP inhibitor JOURNAL Patent: US 6074876-8 5 13-JUN-2000;	a)		,	1 aattacaacggtatatatcctgccagtactcggccgtcgaactcggccgtcgaqtacatg	1 AATTACAACGGTATATATCCTGCCAGTACTCGGCCGTCGAGTACATG 4 61 gtcgataagaaaaggcaatttgtagatgttaattcccatcttgaaagaaa	48 GICGATAAGAAAAGGCAATTIGIAGAIGTTAATTCCCATCTIGAAAGAAATATAGTTTAA 1 121 atatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataaatttatt 1 11111111111111111111111111	FTAT Lgcc 	241 tagatgaaagactgagtgcgatattatgtgtaatacataaattgatgatatagctagc	301 agctcatcgggggatcctagaacgcgtgatctcagatctcggtgacgggacggac	361 ggggcggtaccggcaggctgaagtccagctgccagaaacccacgtcatgccagtt	421 gcttgaagccggccgccagcatgccgcggggggcatatccgagcctcgtgcatgc 4	407 GCTIGAMGCCGGCCGCCGCATGCCGGGGGGGGGGGCATAICCGAGCCCTCGTG 481 gcacgctcgggtcgttgggcagcccgatgacagcgaccacgctcttgaagccctg 482 gcacgctcgggtcgttgggcagcccgatgacagcgaccacgctcttgaagccctg 483 gcacgctcgggtcgttgll	40/ 0chcolloadelcalloadehaccedalgacacacacacacacacacacacacacacacacacaca

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On Jul 29, 2000 this sequence version replaced g1:9186839.
Bases 76,114-90,387 of clone F1019 overlap with bases 1-14,276 of
'IGE' Bac clone F5A8, gblAc004146.
e-mail for correspondence: arab8esquence.stanford.edu
Genes with similarity to proteins in the databases are described as
'putative', '-like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://gonmbio.ornl.gov/section/index.html), GENSCAN (Chris Burge,
http://gonmbio.stanford.edu/-chris/GENSCANW.html), Fexa (V.Solovyev
& A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and
NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).
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I (bases I to 90387)
Federapiel. N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Nguyen, M., Lam, B., Southwick, A., Miranda, M., Brooks, S., Buehler, E., Chao, C., Chiou, J., Choi, E., Gonzalez, A., Howng, B., Johnson-Hopson, C., Khan, S., Kim, C., Koo, T., Lee, J.M., Lenz, C., Liu, A., Liu, S., Mukharsky, N., Pham, P., Sakano, H., Shinn, P., Toriumi, M., Vaysberg, M., Yu, G., Ecker, J., Theologis, A.
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Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
Altafi, H., Nguyen, M., Lam, B., Southwick, A., Bei, Q., Buenhier, E.,
Chin, C., Chiou, J., Choi, E., Dunn, P., Gonzalez, A., Howng, B., Kim, C.,
Koo, T., Lee, J.M., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S.,
Mukharsky, N., Pham, P., Sakano, H., Schwartz, J., Shinn, P.,
Theologis, A., Toriumi, M., Vaysberg, M., Walker, M., Yu, G., Ecker, J.,
Theologis, A. and Davis, R.W.
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Altafi, H., Nguyen, M., Lam, B., Southwick, A., Ecker, J., Theologis, A.
and Davis, R.W.
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Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Arailo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Marker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
Direct Submission
Submitted (24-MAR-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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Submitted (29-UUL-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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Submitted (09-AUG-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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                                                                                                                                                                                                                                         AC007152 90387 bp DNA PLN 09-AUG-2000
Arabidopsis thaliana chromosome I BAC F1019 genomic sequence,
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Arabidopsis thaliana
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Vaflsalqasdghwpgeftgplcmlpplivflyitghleevpdaehrkemlriiychq
Nedgemeftersimpritylnvilliyclygbpgglenarrrargwilshgvyitp
CWGKWLSvlgiydwsgvnpmppeiwllpyfldihlgreffyrmlsylygry
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KHEXRIPDWMWAVAEDGMKWOCKGSQLWMTGFRYDAALLASDPREDTYDYLRKHYIKK
SQYRDNPSGDFKSWYKHISKGWTLSDRDHGWQVSDCTAEAAKCCMLLSTMPDITGE
KINLEQLYDSVNLMLSLQSENGGFTAWEPVRAYKWMELMNPTDLFANAMTEREYTECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLODEQYLVPHTSLVQDAHKAGLQVYVSGFANDVDIAYNYSSDPVSEYLSFVDNGDFS
VDGVLSDFPTTASAAVDCFSHIGRNATKQVPEVLSKOGASOTPRGCTDLAYERAIKD
GADVIDCSVQMSSDGPFECLIS IDLANSIAALQNTFSNRSTSYPEISSYPGIFFFSLY
WPEIQSLTPAISNPFRVYRIFRNPREKNSGKLISLSQFLDLAKTYTSLSGVLISVENA
ATREKGGLOVVQAVLDFLTBAGYSNOTTTFKWNIGSTNSSTYUDFKKKSKYEYETYKI
EETIGNIRDSAIEDIKKFRANAVLNKDSYPENSDSFLJGGTRVWVERLÜKSGLEYVYVI
EFTIGNIRDSAIEDIKKFRANAVLNKDSYPENSDSFLJGGTRVWVERLÜKSGLEYVYVE
FRNEFVSQAYDFFSDATVEINAYIYGAGINGTITEFPFTAARYKRNRCLGREEVPPYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAVLQĀLVIFNQLYDDHRTKEITKSIEKAVQFIESKQLRDGSWYGSWGICFTYCTWFA
LCGLAAIGKTYNNCLSMRDGVHFLLNIQNEDGGWGESYMSCPEQRYIPLEGNRSNVVQ
TAWAMMALIHAGQAKRDLIPLHSAAKFIITSQLENGDFPQQELLGASMSTCMLHYSTY
                                                                                                                                          LRNSIVGLPGVDGLSTEQRKRLTIAVELVANPSIIFMDEPTSGLDARAAIVMRTVRN
TVDTGRTVVCTIHQPSIDIFESFDELLLMKRGGQVIYAGSLGHHSQKLVEYFEAVEGV
PKINDGYNPATWMLDVTTPSMESQMSLDFAQIFSNSSLYRRNQELIKDLSTPPPGSKD
                                                                                                                                                                                                                                                                                                                                 ENEQDLNNFFGAMYAAVLFLGALNAATVQPĀTAIERTVFYREKAAGMYSAIPYAISOV
VACEIMVINGTOTGVYTLILISASMIGCNWMAKFUBAFYYMLISEFIYFTLYGOMLMALTPN
YQIAGICMSFFLSLANHLSGFLIPRPQIPIWRWYWATPVAATLYGILTSQVGDKDS
MVHISGIGDIDLKTLLKEGEGFEHDFLDVVAVVHIAWILLFEFVFAYGIKFLNEQRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNGDAPLVIARGGFSGLYPDSSIAAYQLATLTSVADVVLWCDLQLTKDGLGICFPDLN
LANASTIDRVYPNREKSYSVNGVTTKGWFPNDFSLTELQNFLLIRGILSRTDRPDGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(14858. 14980,15144. 15227,15356. 15436, 15532. 15709,15806. 15996,16096. 16152,16239. 16337, 16424. 15546,16622. 16741,17024. 17137,17221. 17412, 17478. 17644,17746. 17830,17919. 18116,18218. 18307, 18579. 18764,19164. 19367))
// (apen="Figure")
// (continuous figure)
// (continuou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(22449. .22735,22836. .23322,23398. .23540,
23778. .24062,24165. .24203,24289. .24906,25018. .25311,
25570. .25708)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MNSRPSNPTKLVIRSSTLLFCGVVLIHLFAAQIDAQRSTSRWQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLISTIEDVYTTLNREGFWLNVQHDAFYEQQNLSMSSFLLSVSRTVSIDFISSPEVNF
FKKITGSFGRNGPTFVFQFLGKEDFEPTTNRTYGSILSNLTFVKTFASGILVPKSYIL
                                                      DRLQLLRDVGGAFRPGILTALVGVSGAGKTTLMDVLAGRKTGGYIEGSISISGYPKNQ
                                                                                                       TTFARVSGYCEQNDIHSPHVTVYESLIYSAWLRLSTDIDIKTRELFVEEVMELVELKP
                                                                                                                                                                                                                                                                                    VYFKTKYAQSFSTQTKACFWKQYWSYWRHPQYNAIRFLMTVVIGVLFGLIFWQIGTKT
         OKGENRGTEGSVVELNSSSNKGPKRGMVLPFOPLSLAFNNVNYYVDMPSEMKAOGVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 79009 ATATAATGATAACAACAATGAGAACAAGCTTTGGAGTGATCGGAGGCTCTAGGATACATG 79068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atataatgataacaacaatgagaacaagctttggagtgatcggagggtctaggatacatg 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 90387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Putative terpene synthase"
/protein_id="AAF98208.1"
/db_xref="G1:9755447"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 4.2e-248;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1736.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(14858. .19367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(22449. .25708)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAF98209.1"
/db_xref="G1:9755448"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDIFPPWALAEYRKAAFIHHADL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25570. .25708))
/gene="F1019.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F1019.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F1019.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ilarity 99.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Sim
Matches 1739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"Putative protein kinase"
/product-jde"AAP98207.1"
/db xref="G1:975446"
/translation="LFSMSQSLDYQNSCQDSFKVNVPTSFVPEEKEMNLTHLESALRK
GFEKKIVIDELFCQECSSRGTGGFWSTFQ1CCVNVTSLSGGVTVPDPGDPSADELRRR
GSERVSCGNORNLYFFWIPGREXCGHPPFKLDCSGGFAELNTASVNRFILNMSYDSS
NKRLARSDYLNDLCPPNPLNDEPLIETVLQFSADTELLTLYYDCQLNSSATSPFPSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="MAAMLGRDEDPVGALSGRVSLASTSHRSLVGASKSFRDVFMPOT
DEVFGRSEREEDDMELWAATERLEPFEDRLKGRMLPQTSANGKIELEDIDLTRLEPK
DKKHLMEMILSFVEDDNEKFLRDLRBRTDRVGIEVPRIEVRYENISVESDYSKSASRAL
PTLFNVTLNTLESILGFFHLLPSKRKKIQILKDISGIVKPSRMTLLLGPPSSGKTTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLTTGEMLVGPARALFMDEISTGLDSSTTFQICKFMRQLVHISDVTMIISLLQPAPET
BERPDDILLSEGQIYYQGPRDNVLEFEYFCFGCPERKGVAPFLQEVTSKRDQSDVW
NRREQPYRVYVSVDSSGFGFFFFFFFFRYCRTFFRYCRAFTHGAALTYTQKTSNWPET
FKACFDREWLLMKRNSFVYVFKTVQIIIMSLITWTVYLRTEMHVGTVRGGKFYGAMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGELGCDEGRSYYVTRNLSSPLLDRFRGVLNNLREMCKRKVSVPASGPALNTLQTNPN
SNNLKMALEHGFELQDNSNCSMCVLSGGSCGYNQNSSLFVCYCKDGPQDNQCDINLDV
AIIIGIFVALCTIGGFIAFLVLLCPCCKVRIFRNRYTSDDRRQEKLKALIPLKHYTYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MYHLPTSCLVIFFLLSLFHPLPCDSSNQGLGWCETLFQCGNITA
GFPFSGGNRHKECGHPSLELHCNKNNITSLFISNQKYSVLRIDQTSNTLTLAKQNLLG
SFCSSVFTNTTLPPFETFELSRTYKSVTIFYQCSSVLPNLSSYTCPEIGPISVSESPEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QALAGKLDDTLQTCAYISQHDLHFGEMTVREILDFSGRCLGVGSRYQLMSELSRREKE
EGIKPDPKIDAFMKSIAISGQETSLVTDYVLKILGLDICADILAGDVMRRGISGGQKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSLINVMFNGLAELAFTVMRLPVFYKQRDFLFYPPWAFALPAWLLKIPLSLIESGIWI
GLTYYTIGFAPSAARFFRQLLAYFCVNQMALSLFRFLGAIGRTEVISNSIGTFTLLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVKRWTKSFAEVVGRGGFGIVYRGTLCDGRMVAVKVLKESKGNNSEDFINEVSSMSQT
SHVNIVSLLGFCSEGSRRAIIYEFLENGSLDKFISEKTSVILDLTALYGIALGVARGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKADNGDLEHIEIGISSEEEEIAKKMTLVGLMCIQSSPSDRPPWNKVVEMMEGSLDAL
EVPPRPVLQQIHVGPLLESSWITEESSSISEIENRNLQVCEKILS"
complement (1904. .4387)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVFNENLTPGVKCRPPSDSEGSCGYNQTSSTFLCYCKDPYSLSCSSGKSNIRWIIGGV
LILILIVSGIIVSLVFLCLCCRAKIVRKKKSSDALEVPPRPIKESPTLSEDIKART"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTLGGFI IAKDDIRPWMTWAYYMSPWMYGQTAIVWNEFLDERWSSPNYDTRINAKTVG
EVLLKSRGFFTEPYWFWICIVALLGFSLLFNLFYILALMYLNPLGNSKATVVEEGKDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYLHYGCKTRIVHFDIKPQNVLLDDNLSPKVSDFGLAKLCEKKESVMSLMDTRGTIGY
IAPEMISRVYGSVSHKSDVYSYGMLVPEMIGARKKERFGQNSANGSSMYFPEWIYKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YPESCRSSFTVKVPTSFDTKEKELNVTNLESVLRKGFEVTVVINENTCQECLSSLGRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(7942. 8336,8474. 8594,8814. 8902,9019. 9103,
9229. 9462,9545. 9635,9732. 10632,10728. 10888,
11007. 11110,11191. 11356,11443. 11517,11587. 11705,
11797. 12129,12230. 12520,12600. 12683,12759. 12892,
12970. 13197,33273. 13444,13553. 13807,13895. 14164)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="partial coding sequence, 5-prime region of coding sequence extends beyond beginning of this BAC clone."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(2904. .3055,3168. .3194,3282. .3305,3433. .3522,3682. .4387))
//octe="Filol9-2"
//note="Unknown protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Highly similar to PDR5-like ABC (ATP-binding cassette) transporter, gi|1514643 from Spirodela
                                                                                                                                                                                                                                                                                                                                                                                  .1528,1616. .2772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"Putative ABC transporter"
                                                                                                                                                                                                                                                                                                                                                     JOIN(<128. .415,566. .1279,1502.
/gene="F1019.1"

    .90387
    /organism="Arabidopsis thaliana"

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/db_xref="GI:9755445"
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                                                                                                                                     /db_xref="taxon:3702"
Location/Qualifiers
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/gene="F1019.3"
                                                                                                                                                                                                                                                                                                                                 /gene="F1019.1"
                                                                                                                                                                                           /chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F1019.2"
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                                                                                                                                                                                                                                   /clone="F1019"
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O. D.	106	cccttatcggcttg 1119
0y 0b	1120 79189	O aacogctggaataatgccacgtggaagataattccatgaatcttatcgttatctatgagt 1179
o o	1180	gaaattgtgtgatggtggagtggttgcttgctatttacttgcctggtggacttggcct 1239
o o	1240 79309	ttoottatggggaatttatattttaottactatagagotttoatacottttttaoott 129
Qy Db	1300 79369	ggatttagttaatataatggtatgattcatgaataaaaatgggaaatttttgaatttg 1359
Oy D	1360	tactgctaaatgcataagattaggtgaaactgtggaatatatttttttt
92	1420 79489	caaatttgcctttactagaattataaatatagaaaatatataaaatcattcaaataaaaa 1479
දු පු	1480 79549	tgaaaataagaacttcoaaaaaacagaactatgtttaatgtgtaaagattagtogcacat 1539
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9 9	1600 79669	aataaactaaagagtccacgaaaatattacaaatcataagcccaacaaagttattgatca 1659 - - - - - - - - - - - - - - - - - - -
Oy Dp	1660 79729	aaaacttctcaagtctccat 1719
Q qq	1720 79789	tctttctgggc 177 ctrrctgggc 798
oy ob	1780 79849	ctgtcttcccaacctcctacatcacttccctatcggattgaatgttttacttgtaccttt 1839
oy og	1840 79909	ttgtgaaaactaatagggttaacaatcgaagtc 1899
g g	1900 79969	atggaatatggatttggtccaagattttccgagagctttctagtagaagcccatcacca 1959
o o	1960 80029	gaaatttactagtaaaataaatcaccaattaggtttcttattatgtgccaaattcaata 2019
Qy Dp	2020	aattatagaggatatttcaaatgaaaacgtatgaatgttattagtaatggtcaggtaag 2079

Arabidopsis thaliana
Eukaryota; tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Serassicaceae; Arabidopsis.
Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 101933)
Federspiel, N. A., Palm, C. J., Conway, A.B., Kurtz, D.B., Conway, A.R., Au, M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Ojio., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M.,
Vestekala, V.S., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Submitted (31-JUL-1997) Blochemistry, Stanford University/DNA Sequencing and Technology Center, 855 California Avenue, Palo Alto, 2 (bases I to 101933)
Stederspiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Au, M. Araujo, R., Brendel, V., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. 80268 3 (bases 1 to 101933)
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AC004146 GI:3540210 acaaaaatttgggatctactatatatatataatgctttacaacacttggatttttttg Direct Submission CA 94304, 80689 GTG 80691 2620 gcg 2622 VERSION KEYWORDS SOURCE ORGANISM 2140 DEFINITION AC004146 LOCUS REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS TITLE JOURNAL ACCESSION REFERENCE AUTHORS RESULT q QQ δλ ò g δ q QQ δý οy qq ò g g ò ò ò

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COMMENT

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// Procein_id="Aad10659.1"

// Ab_xref="G1:4204278"

// Ab_xref="G1:420478"

// Ab_xref="G1:420
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18665. .18947))
/gene="F5A8.3"
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                                                                                                                                                                                                                                                                                                                                                                         FederSpiel.N.A. Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Au, M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Osborne, B.I., Shina, P., Sun, H., Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J. Theologis, A. and Davis, R.W. Direct Submission
Submitted (30-JAN-1999) DNA Sequencing and Technology Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Sep 4, 1998 this sequence version replaced gi:2934888.
Bases 90722-101933 of clone F5A8 overlap with bases 114738-103537
of 'IGF' BAC clone F1N21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="ribulose bisphosphate carboxylase, small subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted (30-JAN-1999) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
                                                                                                                               ONA Sequencing and Technology Center,
California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(2057. .2293,2430. .2564,2671. .2841))
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/product="ribulose bisphosphate carboxylase, small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /EC_number="4.1.1.39"
/note="Location of EST gb|AA042768. atslA gene
Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organisme="Arabidopsis thaliana"
/cultivare="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .7582,7740. .8251)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(15428. .18947)
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/db_xref="GI:4204274"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 1. 101933
       Yu,G., Ecker,J., Theologis,A
Direct Submission
Submitted (04-SEP-1998) DNA
                                                                                                                                                                                                      Stanford University, 855
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/gene="F5A8.2"
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                                                               TITLE
JOURNAL
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AUTHORS
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JOURNAL
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20045. 26054,26197. 26552,26554. 26688,26776. 27054,776. 27166. 27384,27459. 275617,27707. 27928,28018. 280251,28038. 28049, 288551,28684. 29081,29141. 29297,29386. 29584,29855. 28749,28844. 29901,29141. 29297,29386. 29584,29855. 28749,429894. 29984,29992. 30104,30235. 30310,3151. 31584,31660. 31761,31889. 31084,31150. 31269,31551. 31584,31660. 31761,31889. 32071,32153. 33238,33405. 33494,33957. 34094,34133. 34228. 34305. 334494,33957. 34094,34133. 34228. 34305. 33494,33957. 34094,34143. 34228. 34305. 33414,3414,3414,4411. 41465,41548. 41741,41894. 42199,42289. 42293,41162. 44931,45058. 45180,45129,46501. 46101,41411. 41465,41548. 47721,4745. 47614,48094. 4766,48379. 48463,48588. 48588. 48913,
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RHFLEKYRDAVWDVNSFSEPFEIHSRVKKSFEMVSLAVSQKRPVLLYGPSGSGKSALI
RKLADESGNHVVFIHMDDQLDGKTLVGTYVCTDQPGEFRWQPGSLTQAIMNGFWVVLE
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TTT LVQULLAHT GQKLTVLNLSQQSDTVDLLGGETGTE RTATLOQULANGTMVYTMCTMVTBENELABLK
IKTLVQOLLAHT GGKLTVLNLSQQSDTVDLLGGETF IDENGTTGTARSRENGTK
KPEELK NCACLRTKVNK IRQQ IHSGGMVFTFVEGAFVTALREGHWYLLDEVNLAPPE
ILGRLIGVLEGVRGSLCLABRGDWOLF IPRHLENETRACMPATDAGRADLFSFRSRF
TEX AVDDITCDDDLEFTVRRELGGRSSDSK IVANIVMFYKEARRISESESLQDGANQKP
OYSLRSLYRALEYARLGGRSSDSK IVANIVMFYKEARRISESESLQDGANQKP
OYSLRSLYRALEYA IKABAIGGFQKALYDGFSMFFLSLLDASSAK I VEPIIKRISGEN
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PFFISKGDENPEIGGFEFLAPTTHRNVLRVLRAMOLSKPILLEGSPGVGKTSLILALG
KYSGHKVVRINLSEQTDMMDLLGSDLPVESDEDMKFAWSDGILLOGLNAILDHRAQYF
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VIHALGDAFLHPEFTVPLVHCFLPIIRNVVDRVVGLLRLVDDLKSSIDYSDDVSSVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLSPLWRRIVVYPPDRESLQSILGARŸPNLGPVAEKLÏETFETINSALRPQFSSSTTE
NSATFSSPSRFSLRDLLKWCERVHGLPSYDGHAVYQEAADIFSASNMSVKNRVAVSEI
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WFNRLHTGRTLTVRDLLSWVAFVNMATESLGPAYAILHGAFLVLLDGLSLGTGFSGRD
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GYPLNELNLSSATDSSDLLGCFEQYNAFRNFRLVWTRVEHLVDEYNSLLLQSSQEALF
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SKKYLEQISKTILQLQTHEKKQSTKFEWVTGMLIKAIEKGEWVVLKNANLCNPTVLDR
INSLVEPCGSITINECGIVNGEPVTVVPHPNFRLFLSVNPKFGEVSRAMRNRGVEVFM
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RKNLKFLCRLDPDAVPIPMLSSKLIDVAASNDQSKPYSKSLFESLNSVGVLRRSYQQW
LVESNDNHTDVSTFTRFLDSLRVLEKKILCEIVGAPSFSVLIQLYTEVIDNHSFFWSG
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MAFEDIKLGDLIIPKGLSIWIPVLAIHHSNELWGEDANEFNPERFTTRSFASSRHFMP
                                                               FAAGPRNCIGQTFAMMEAKIILAMLVSKFSFAISENYRHAPIVVLTIKPKYGVQLVLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40066. .40139,40861. .41011,41411.
41894. .42199,42289. .42393,43162.
45259. .45432,45649. .45768,45852.
46101,46660. .46738,46894.
47445. .47614,48094. .48266,48379.
                                                                                                                                                                                               .49118)
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                                                                                                                                                                                                                                                                                                                                      complement(join(23319.
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                                                                                                                                                                                               complement(23318.
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                                                                                                                                                                                                                                                                      /gene="F5A8
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IVSSSDEYLLESEWALIKSIKKMHSFEPGEWOUVLEESKNINNIVLHGHPEKSMLMAY
GCHPSLPVSAELFHKOQEFLQLCSTVWPLKSESDEHONDHITKAIPPSGPELCLLALE
GLCISSYTANDEDDYDYVAAVQLEIRYLEKKREDKMGFSEIDMTENITAS
CCYFCPELYTTGSGFSGWYWTCPIASSESCSLDVELLAALQHILLVARPTEHQLDLUNDIR
KLIKPALEYSTSAEDDYDYVAAVQLEINATDAHASELGVDTKTAGFSEIDWTWHYSVL
WNNSQIGHMIAHLTGSFFHLMPFGPEVLEHWQLSDSYPTFADASCENSYRCSDSITY
THQKSFESETPVAIKSYFHALEKQNKMDGTONLISLIGSSSHNKLKSVTHSFVGPIA
KRLYSDSSNEFYCNLGLAWLYIGGLRFHLLNSLDVIDPAMITTCKLLKLEEKISSLL
LNIKVRGEGSTLGGLLYSGNNDESSEBHTGKTKTERKTQRKVTERSDFKXYDDLRRA
LDEFAGFLTRISLANDISSSBHTGKTYRTHARPKORVYTERSDFKXYDDLRRA
LDEFAGFLTRISLANDISSSBHTGKTYRTHARPKORVYTERSDFKXYDDLRRA
LDEFAGFLTRISLANDISSSBHTGKTYRTYRTHARPTORY
QVSVYEWKLGLSLFVSGALLGKLLNRPDIDWVDSVWETIYALMRFPRDSSTAFTYTE
CLPPLHISHGANSRARSIGLDVGLLIKTLISVSSAEDSFKABLOLGKYALKYRLHARVL
QFVANYGLLDBASFELLDRIY IVVELARTWMWKFQAKTKADNLYGLYFRSRDFKTDSY
IVSTHWELGFCDCDLSEKTIYSTGSGRFCTIPDSRLDSFTDSYELGKYALKYFTSFPHK
VSFLKUCHSTSFSENDYSSSRYNYKOUTHINGOFELGKWYFTTPLQQFIN
SLLQRREDHFGLQKLSGVLQMLLAIPSSTPLAKALSGLQFLLCKVYHKLOEGGCKLDTS
SLLQRREDHFGLQKLSGVLQMLLAIPSSTPLAKALSGLQFLLCKVYHKLOEGGCKLDTS
SLLQRREDHFGLQKLSGVLAPPELDTGJTSONLYFDSRSSKRYNKFONNYKKITSFPHK
VSFLKOLKGLYYKKLITKRSYGFFRLLNTATORYONTHIF
GFYIQFLDVVWGQLDLNRKNYFTLLMGABHQYSSRYYGTNYRTHTSRTRTRORVYKKLITG
KFTDMLELDVWHGCLDLNRKNYFTLLMGABHQYSSRYYGTNYRTHTSRTRGTTAG
CSDLMRNSDRDVAKKRALFELLKLLESSGLQKHKFENIEMSNYTVRTTSCRYTART

0; 1119 1179 3077 3137 3437 tactgotamatgoataagattaggtgaaactgtggaatatatattttttoatttaaaag 1419 666 3377 0; Gaps 12; Length 101933; atataatgataacaacaatgagaacaagctttggagtgatcggagggtctaggatacatg aaccgctggaataatgccacgtggaagataattccatgaatcttatcgttatctatgagt 4; Indels Score 1736.6; DB 12 Pred. No. 4.1e-248;); Mismatches 4; ;0 29.6%; 99.8%; Best Local Similarity 99.8 Matches 1739; Conservative Query Match 2838 940 2898 2958 1060 3018 1120 3078 3138 3198 3258 1000 1180 1240 1300 1360 3318 1420 3378 q g ð à ò a Q ð ò g ç g ò 8 ò g à Q ð 8

3497

Qy	1540 3498	caagtcatctgttacaatatgttacaacaagtcataagcccaacaagttagcacgtcta 15
oy Op	1600 3558	aataaactaaagagtccacgaaaatattacaaatcataagcccaacaaagttattgatca 16
Qy Db	1660 3618	aaaaaaaacgcccaacaagctaaacaagtccaaaaaaaattctcagtctccat 17
Qy Db	1720 3678	cttcctttatgaacattgaaaactatacacaaaacaagtcagataaatctcttctgggc 17
Qy	1780 3738	acttccctatcggattgatgttttacttgtacctt 18
Qy Db	1840 3798	gtgaaaactaatagggttaacaatcgaagtc 18
QY	1900 3858	ittctagtagaagcccatcacca 19:
Qy	1960 3918	attatgtgccaaattcaatat 20.
Qy Db	2020 3978	ttattagtaaatggtcaggtaag 207
ço ga	2080	ccagtgtggaattgt 213
Qy Db	2140	Ugctttacaacacttggattttttttg 2
Oy Db	2200	vatgcaccaactcattgtttagtg 225
Oy Db	2260 4218	ttgtcaaatatatgttcgtgtatatttgtataagaatttctttga 231
Qy Db	2320	atatatattatatatatcatgcacttttaatt 237
Qy	2380	.atatatatagtgcatttttctaacaaccatatatgttgcgattg 243
QY	2440)ctagagtaatgaaaaatataatctattgctgaaattatctcaga 249
Qy	2500 4458	ttaagattttettaaagtaaattetteaaattttagetaaaagtettgtaataaeta 255
Oy Dp	5 5	acaatctcgaccacggaaaaaacacataataaatttgaatttcgacc 261
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/gene="ats1A"
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Matches 1733; Conserv
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                                                                                                Query Match
                                        BASE COUNT
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Example 22, B-9000 Gent, Belgium

ats1A is one of four Rubisco small subunit genes found in

Arabidopsis thaliana. While the other three genes (see <ATRBSCB>)

are closely linked in a tandem array, ats1A is at least 10kb

removed from, or completely unlinked to, the three B subfamily
genes. The B subfamily genes are more similar to each other than tats1A in nucleotide and amino acid sequence. The 5' flanking
sequences of the ats1A gene have been used to express chimeric
genes in transgenic tobacco plants (be Almeida et al., Molec. Gen.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MASSMLSSATWVASPAQATWVAPFNGLKSSAAFPATRKANNDIT
STSNGGWWYWPYDFGKKKFFTLSYLPDLTDSELAKFVYLIRNKWIPCVEFE
LEHGFVYRBHGNGGYYDGRYWTWMKLPLFGCTDSAQVLKEVEDECKKEYPNAFIRIIG
FDNTRQVQCISFVAYKPPSFTG"
                                                                                                                                                                                         join(1732. .1902,1897. .1902,2009. .2143,2280. .2516)
/gene="ats1A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Join(1897. .1902,1897. .1902,2009. .2143,2280. .2513)
                                                                              ATRECSA 2821 bp DNA PLN 09-JUN-1999 Arabidopsis thaliana atslA gene for ribulose 1.5-biphoshate carboxylase small subunit (EC 4.1.1.39).
                                                                                                                       X13611 X14565
X13611.1 G1:16452
rbcs multigene family; ribulose bisphosphate carboxylase
thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="ribulose bisphosphate carboxylase"
/protein_id="CAA31948.1"
/db_xref="G1:295792"
/db_xref="SWISS-PROT:P10795"
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             Seurinck,J., Truettner,J. and Goldberg,R.B.
The nucleotide sequence of an anther-specific (
Nucleic Acids Res. 18 (11), 3403 (1990)

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Data kindly reviewed (13-DEC-1990) by Mariani (
Location/Qualifiers
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Nicotiana tabacum
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Nicotiana.
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                              tctatcgagagatagattgaaagaagtgcagggaagcggttaactggaacataacacaat 4200
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ACAGATTGTTACATGGAAAACAAAAGTCCTCTGATAGAAGTCGCAAAGTATCACAATTT 755
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                                             gtctaaattaattgcattcgctaaccaaaaagtgtattactctctccggtccacaataag
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Direct Submission
Submitted (23-MAR-1990) Mariani T., Plant Genetic Systems,
Plateaustraat 22, B 9000 Gent, Belgium
2 (bases 1 to 6254)
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ORI	IGIN	574 ATTIAATTATTTTTTTACTACAGTGCCCTTGGAGTAAATGGTGGAGTATGTGTTAGA
JEE	Query Match 25.8%; Score 1512.2; DB 14; Length 6254; Best Local Similarity 99.8%; Pred. No. 9.4e-215; Matches 1514; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	4381 aatgittatgigaagaatagitaaaggitaatatgatcaatitcattgctatttaatgit
ç,	3361 ggtaccatggtagctaatttctttaagtaaaactttgatttgagtgatgatgtgtact 3420 	Oy 4441 aaaatgtgaatttottaatotgtgtgaaaacaaccaaaaatcacttattgtggaccgga 4500
Q D	2) gttacacttgcaccacaagggcatatatagagcacaagacatacacaacaactgcaaaa 348 	Qy 4501 gaaagtatataaatatatttggaagcgactaaaaataaactttctcatattatacga 4560
OY Db	ttgttggagcatttcgaggaaalgggagtagcagctaatctgaggtaac 354 	Oy 4561 acctaaaaacagcatatggtagtttctagggaatctaaatcactaaaataaaagaa 4620
Oy Dp	3541 attaaggtttcatgtattaatttgttgcaaacatggacttagtgtgaggaaaagtacca 3600 	Oy 4621 gcaacaagtatcaatacatatgatttacaccgtcaaacagcgaaattcgtaaatatttaat 4680
Qy Dp	tgtctcaccctgatttcagttatggaaattacattatgaagctgtgctagagaa 366 	Oy 4681 ataataaagaattaatccaaatagcctccacctataacttaaactaaaataaccagc 4740
S S	gccacccacttatgcaagtctgcttttagctt 	Qy 4741 gaatgtatattatatgcataatttatatattaaatgtgtataatcatgtataatgt 4800
Oy Dp	1 actgatttaatttacattgctaaatgtgcatacttcgagcctatgtcgctttaattcgag 378 	Oy 4801 ataatctatgtatatggttagaaaagtaaacaattaatatagccggctatttgtgtaaa 4860
o d	ataaagtgacaa 384 ATAAAGTGACAA 105	Oy 4861 aatccctaataatcg 4877
Qy Db	3841 gtcaattgtccttcttgtttggcactatattcaatctgttaatgcaaattatccagtta 3900 	
Q Q	3901 tacttagctagatatccaattttgaataaaaatagctcttgattagtaaaccggatagtg 3960 	TION PVE108 ION A23334 N A23334 DS
O _Y	3961 acaaagtcacatatccatcaacttctggtgctcgtggctaagttctgatcgacatgggg 4020 	Escherichia M Plasmid Esch Bacteria; Pr Escherichia
δ O	4021 ttaaaatttaaattgggacacataaatagcctatttgtgcaaatctccccatcgaaaatg 4080 	REFERENCE 1 (DASES 1 tO 5620) AUTHORS TITLE STAMEN-SPECIFIC PROMOTERS FROM RICE JOURNAL PAtent: WO 9213956-A 9 20-AUG-1992;
ç q	4081 acagattgttacatggaaaacaaaagtcctctgatagaagtcgcaaagtatcacaattt 4140 	FEATURES LOCATION/QUAINTIERS 15520 /organism="Escherichia coli" /plasmid="pvE108"
oy G	4141 tctatcgagagatagattgaaagaagtgcagggaagcggttaactggaacataacacaat 4200 	
oy O	4201 gtctaaattaattgcattcgctaaccaaaaagtgtattactctctcggtccacaataag 4260 	/note="Agrobacterium T-DNA derived sequence; contains polyA site from nopaline gene" 11391683 /note="tapetum-specific; Nicotiana tabacum derived
Q D	4261 ttattttttggcccttttttatggtccaaaataagtgagttttttagatttcaaaatg 4320 	sequence" 16842516 √note="1583; Califlower mosaic virus isolate CabbB-JI derived sequence"
ογ	21 atttaattattttttactacagtgcccttggagtaaatggtgttggagtatgtgttaga	gene 25173068 /gene="bar" CDS 25173068

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                   taaaaactttgatttgagtgatgatgttgtactgttacacttgcaccacaagggcatata
                            tagagcacaagacatacacaacaacttgcaaaactaactttgttggagcatttcgagga
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Pred. No. 6.1e-179;
); Mismatches 11;
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Williams, M. and Leenans, J.
Maintenance of male-sterile plants
Patent: US 5750867-A 3 12-MAY-1998;
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Sequence 3 from patent US 5750867
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Best Local Similarity 98.9%;
Matches 1291; Conservative (
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FWTDDLVRLRERYPWLVAEVDGEVAGIAYAGPWKARNAYDWTAESTVVVSPRRQRTGL
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VGFWQLDFSLEVVPPREVLPVTEI"
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/note-"Agrobacterium T-DNA derived sequence; contains
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                                                                                                        POLYA site from nopaline synthase gene" 3357. 5620
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Pred. No. 6.1e-179;
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Similarity 98.9%; Pred. No. 6.1e-179;
1; Conservative 0; Mismatches 11;
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Williams, M. and Leemans, J.
Maintenance of male-sterile plants
Patent: US 597433-A 3 02-NOV-1999,
Location/Qualifiers
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                                                            Sequence 3 from patent US 5977433.
AR084079
AR084079.1 GI:10010850
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score greater than or equal to
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Plasmid pTCO113 (AAT39339) is a T-DNA vector containing a bar gene under control of the PSSU promoter, a barnase gene under control of the stamen-specific PTA29 promoter, and a barstar (co-requilatory) epiene under control of the Pnos promoter. 87% of oilseed rape plants regenerated after Agrobacterium-mediated transformation using pTCO113 were male sterile. Barnase expression disturbed the expression of stamen cells leading to male sterility. Constitutive expression of barstar counteracted any low level expression of
                                              /note= "region containing polyA signal of nopaline synthase gene of Agrobacterium T-DNA" complement (3032..3367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                        of
                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                         gene
                                                                                                                                                                                                                                 οĘ
                                                                                                                                                                                                                                                                                          of Bacillus
                                                                                             /label= Barnase
/note= "Bacillus amyloliquefaciens barnase
                                                                                                                                                                                                                                 synthase gene
                                                                                                                                                                                                                                                                                                                                                                                                       "left border of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                   of
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                                                                                                                                                                       stamen-specific TA29
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//abel= 3/g7
/note= "region containing polyA signal of Agrobacterium T-DNA"
complement (5840..5864)
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amyloliquefaciens"
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                                                                                                                                                                                 Nicotiana tabacum
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             complement (2659..3031)
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  subunit gene'
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/label- Pnos
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/label= 3'
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             polyA_signal
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99.7%; Score 5849.8; llarity 99.9%; Pred. No. 0; Conservative 0; Mismatches

Query Match Best Local Similarity Matches 5862; Conserv

DB 17; Length 5864;

220 catattedtatagectta 221 catattegttttggccat 220 catattegttttggccat 220 catattegttttggccat 2281 tatatgettegtgtata 2280 tatatgettegtgtata 2280 tatatgettegtgtata 2340 tatatatatatatatatt 2340 tatatatatatatatatt	2401 atagtgcattttttctaacaa	ccggggatettecc 	2941 tgaaattgaccgatcagag 2941 tgaaattgaccgatcagag 2940 tgaaattgaccgatcagag 1111111111111111111111111111111111	3121 aagcctgatgtatagtaata 3121 aagcctgatgtatagttaata 3120 aagcctgatgtatagttaata 3181 ttgccttcctgtttgagaag 1180 ttgccttcctgtttgagaag 3180 ttgccttcctgtttgagaag 3181 ttgcttcctgtttgagaag 1181 ttgcttcctgtttgagaag 1181 ttgcttcctgtttgagaag 1181 ttgcttcctgtttgagaag
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83.6%; Score 4903.2;
larity 99.9%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                               /note= "T-DNA left border"
 complement (3032..3367)
                                                                                                                                                                                                                                                                                                                        Example 3; Page 13-16; 25pp; English.
                               /product= barnase
                                         complement (3368.
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                     /label= Barnase
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PTA29
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Matches 4916; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                      Transgenic plant; poly-(ADP-ribose) polymerase inhibitor; PARP; niacinamide; Agrobacterium; T-DNA; male sterile; barnase; ribonuclease; RNase; cereal; wheat; ollseed rape; Brassica napus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   poly-A
T-DNA"
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gene of Arabidopsis thaliana"
complement (2658..3031)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "3'untranslated region contg. the poly-A signal of the nopaline-synthase gene of Agrobacterium T-DNA"
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complement (883..2608)
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                                                                                                                                                                                                                                                  occoagatotgcatggagccatttacaattgaatatacctgccg 5865
                                                                                                                                                                                                                                                             /note= "T-DNA right border" complement (97..330)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (1..25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric Agrobacterium sp.;
Chimeric Arabidopsis thaliana;
Chimeric Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                       AAT59531 standard; DNA; 4946
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/label= 3'97
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/label= 3
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9 plasmid pTHW107 is a vector carrying T-DNA (AAT59531) comprising a barnase coding sequence under control of the tobacco TA29 gene stamen specific promoter and a phosphinothricin acetyltransferase coding sequence under control of an Arabidopsis Rubisco small subunit gene promoter. Oilseed rape hypocotyl explants were subunit gene promoter. Oilseed rape hypocotyl explants were pTHM107 and helper Ti plasmid pMP60. In some treatments, the hypocotyls were treated with the poly-(ADF-ribose) polymerase inhibitor niacinamide (250 mg/1) 4 days prior to infection. Plants reagenerated from miacinamide-treated transformed calli had a low copy number and displayed less variation in the expression profile of the transgenes. rroun. of transgenic plants using a poly-(ADP-ribose) polymerase inhibitor – reduces the cultured cells response to stress and reduces metabolism DB 18; Length 4946; /note= "promoter region of tobacco TA29 gene" complement (4822..4946) 3; Indels Sequence 4946 BP; 1569 A; 891 C; 963 G; 1523 T; 0 other;

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Qy	1921	agatttccogagagctttctagtagaagcccatcaccagaaatttactagtaaaataaa 1980
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ataataaagaattaatccaaatagcctcccaccctataacttaaactaaaaataaccagc 4740
      gaatgtatattatatgcataatttatatattaaatgtgtataatcatgtataatcaatgt
                                    Transformed plant cell with disrupted metabolism · from a proby foreign male-sterility DNA inserted in the nuclear genome
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AAN92188 standard; DNA; 3265
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Best Local Similarity 99.7
Matches 1513; Conservative
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Score 1500.2; DB 10; Length 3265; Pred. No. 3e-242; 0; Mismatches 3; Indels 1;

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                                                                        gcaacaagtatcaatacatatgatttacaccgtcaaacacgaaattcgtaaatatttaat 4680
                                                                                                      4681 ataataaagaattaatccaaatagcctcccacctataacttaaactaaaaataaccagc 4740
                                                                                                                                       gaatgtatattatatgcataatttatatattaaatgtgtataatcatgtataatcaatgt 4800
                                                                                                                                                                                                                                                                                                                                                                                                                                     13' regulatory region from T-DNA nopaline synthase gene of Agrobacterium containing the polyadenylation site"
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synthase gene of Agrobacterium containing the
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/note≂ "Nicotiana tabacum tapetum specific promoter"
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3069..3356
                                                333 ACCTAAAAACAGCATATGGTAGTTCTAGGGAATCTAAAATCACTAAAATTAATAAAAGAA
                                                                              93 ATAATCTATGTATATGGTTAGAAAAGTAAACAATTAATATAGCCGGCTATTTGTGT-AA
                                                                                                                                               Immature; spikelet; microsporocyte; meiosis; anther; probe; leaf;
                                                                                                                                                                                                                                                                                                                                     expression cassette, root; stamen; fertile pollen; barstar; PT72 35S3; nos; Agrobacterium; pVEI08; pTSX11; pTSX11-T72; pJVR1-T72; PCR; polymerase chain reaction; amplify; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35S3 promoter sequence from Cauliflower mosaic virus isolate CabbB-JI"
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/note= "pUC18-derived sequence"
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plant transformation vector which contained both the barstar-encoding DNA under the control of the tapetum-specific PT72 promoter (see AAQ27486) and the herbicide resistance gene, bar, under the control of the tapetum-specific PT72 promoter (see AAQ27486) and the herbicide resistance gene, bar, under the control of the 3553 promoter. This vector can be used for the transformation of rice and corn. The 3' untranslated end of the nos gene of Agrobacterium T-DNA was amplified using the primers given in AAQ28021-2. The reaction product was ligated to the large fragment of pVE108 which had been cleaved with EcoRI and NcoI to yield plasmid pTSX11. A from plasmid pMT416 using the primers given in AAQ28023-25. The final reaction product contained the barstar coding sequence under the control of the PT72 promoter and two linker sequences, the 5' linker control of the PT72 promoter and two linker sequences, the 5' linker control of the PT72 promoter and two linker sequences, the 5' linker containing restriction sites for MSCI, NcoI, NHeI and NoII and the 3' linker containing a BSTEII restriction site and a 3 nucleotide spacer (GGG). This fragment was ligated into NcoI and BStEII digasted PTSX11 to yield bJVR1-T72. The 3553 promoter containing fragment was amplified from pDE9 using the primers given in AAQ28026-27. The reaction product was ligated to NcoI and NheI digested PTSX11-T72 to yield bJVR1-T72. This plasmid can be used to provide gene expression in the other parks of a plant, and do not provide gene expression in the other parks of the plant that are not involved in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 5620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for producing male-sterile or
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98.8%; Pred. No. 1.6e-203;
iive 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scheirlinck
                                                                                                /*tag= h
/note= "pUC18-derived sequence"
polyadenylation site"
3357..5620
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91EP-0402590.
91EP-0403352.
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Matches 1290; Conservative
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10-DEC-1991;
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BP.

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AAQ53875 standard; DNA; 5620
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                               cogcogatgottttccccggagcgacgtctgcaaggttcccttttgatgccacccagccg
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promoter sequence derived from
lower mosaic virus isolate CabbB-JI."
                                                           hybrid;
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                                   Plasmid pVE108 used in the construction of plant maintainer gene.
                                                                                                                                                                         '3' regulatory sequence containing the polyadenylation signal derived from the nopaline synthase gene from Agrobacterium
                                                                                                                                                                                                                                                                                       specific
                                                     Maintainer gene; sterile; sterility; homogenous population; seed; fertility restorer gene; pollen lethality gene; ds.
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Bacillus amyloliquefaciens."
complement (1139..1683)
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acetyltransferase gene."
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/label= pUC18.
/note= "pUC18 derived sequence.
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promoter of Nicotiana
1684..2516
                                                                                                  Location/Qualiflers
1..395
/*tag= //tabel= pucl8
//note= "pucl8 derived secomplement (396..802)
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/label= TA29.
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/label= 3'
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misc_feature
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                  27-JUN-1994
                                                                                                                                               misc_signal
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03-NOV-1992;
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                                                                                Synthetic.
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DNA; 5349
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                                             comprises (a) a ferility restorer gene which comprises a fertility restorer DNA and (ii) a restorer promoter capable of restorer DNA and (ii) a restorer promoter capable of directing the expression of the fertility restorer DNA and (b) a pollen lethality gene that is selectively expressed in microspores and/or pollen of the plant to prevent the production of functional pollen specific promoter capable of directing expression of the pollen lethality DNA. Plants transformed with this DNA (maintainer plants) can be used to maintain a homogenous population of male certile plants for the production of hybrid seed. This plasmid contains DNA encoding Barnase (the pollen lethality DNA), the TA29 tapetum-specific promoter (the restorer promoter) and phosphinothricin acetyl transferase under the control of the 35S3 promoter. It was used alongside another plasmid (pVE144, described in the ADS5387) in the construction of a plant transformation vector
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 gene for maintenance of male-sterile plants - fertility-restorer gene and pollen-lethality gene
                                                                                                                                                                                                                                      Sequence 5620 BP; 1499 A; 1362 C; 1324 G; 1431 T; 4 other;
                                                                                                                                                                                                                  comprising a maintainer gene as described.
                             Example 2; Page 55-58; 87pp; English
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 1289; Conserv
  Maintainer
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/note= "region containing
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/label= RB
/note= "right boarder"
complement (98..331)
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low fidelity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 atatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataaatttatt 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A encoding an improved barstar protein - used to restore fertility male-sterile plant lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 aattacaacggtatatatcctgccagtactcggccgtcgaactcggccgtcgagtacatg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09
                                                                                                                                                                                                                                                                                                                                                                   The present sequence was used in the preparation of an improved Barillus amyloliquefaciens barstar, i.e. barnase inhibitor, which can be used to restore fertility to male-sterile lines. The DNA sequence encoding the improved barstar, leads to increased barstar production in tapetum cells, due to improved translation,
          /note= "region coding for phosphinothricin acetyl
                                            /label= P35S
/note= "35S promoter of Cauliflower Mosaic Virus"
2281..3969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
                                                                                         of rice (WO9213956)'
                                                                                                                                         /label= 3'_chs
/note= "region containing 3' untranslated end
chalcone synthase gene"
complement (5325.5349)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.1%; Score 885.8; DB 19; Length 5349; llarity 99.8%; Pred. No. 1.7e-139; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5349 BP; 1339 A; 1233 C; 1290 G; 1487 T; 0 other;
                                                                                      'note= "promoter of El gene
                                                                                                                                                                             /*tag= h
/note= "T-DNA left border"
                                                                                                                  improved_barstar
                            complement (884..2258)
                                                                                                                                                                                                                                                                                                                                                    Example 4; Pages 41-43; 54pp; English.
                      transferase
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                                                                                                                                                                                                                                                                                                                                                                                                               possibly protein stability.
                                                                                                                                                                                                                                                                         (PLBZ ) PLANT GENETIC SYSTEMS
                                                                      /*tag= e
/label= PE1
                                                                                                                                                                                                                                        97WO-EP04739
                                                                                                                                                                                                                                                        96EP-0202446
                                                                                                                                   'label= 3'
                                                                                                .4245
                                                                                                                           246..4577
                                                                                                                  product-
                                                                                                                                                                                                                                                                                           Ξ
                                                                                                                                                                                                                                                                                         Williams
                                                                                                                                                                                                                                                                                                          WPI; 1998-193630/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                    misc_feature
                                                                                                                                                                                                     WO9810081-A2
                                                                                                                                                                                                                                                       03-SEP-1996;
                                                                                                                                                                                                                                                                                         Michiels F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Simi
Matches 887;
                                                                                                                                                                                                                     12-MAR-1998
                            promoter
                                                             promoter
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420
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                                                                                                                                                                    999
                                                                                                                                                                                                                       plant; mutant barnase gene; anther-specific expression; PCR; primer; plant breeding; ss.
                                                 ageteategggggatectagaacgcgtgateteagateteggtgaegggaeeggae
                                                                                                                                           gggagacgtacacggtcgactcggccgtccagtcgtaggcgttgcgtgccttccaggggc
                                                                                                                                                                       ccagggacttcagcaggtgggtgtagagcgtggagcccagtcccgtccgctggtggcggg
                                                                                                                                                                                                                                                                              E. coli plasmid pTS431 containing mutant barnase gene.
                                                                                                                                                                                                                                                                                                                       AAZ91097/c
ID AAZ91097 standard; DNA; 6539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-0220060.
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Fri Nov 16 16:21:39 2001

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5811 CGGAAGTTGACCGTGCTTGTCTCGATGTAGTGGTTGACGATGGTGCAGACCGCCGCGCATG 5752
                                                                                                                                                                                                                  male sterile; barnase; ribonuclease; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cauliflower mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function= region containing polyadenylation signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                                                                                                                                                                polyadenylation signal
                                                                                                                                                                                                                                                                                                                                                                                             gene of Agrobacterium
                           E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphinothricin acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stamen-specific
                                                                                                                                                                                                                                                                                                               /label= vector
/note= "pUC19 derived vector sequences"
complement (2019..2283)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product- Bacillus amyloliquefaciens complement (2625..4313)
                                                                                                                                                                                         sterile rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function= promoter of the of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function= 35S promoter of
                                                                                                                                                                                                                                                                                                                                                                               /note= "region containing
nopaline synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                  complement (2284..2624)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Michiels
                                                                                                                                                                                                                                                                            Location/Qualifiers
1..2003
                                                                                                                                                                                         to obtain male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ≥
                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Barnase
                                                                                                                                                                                                                              rice; Oryza sativa; ds; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PLBZ ) PLANT GENETIC SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                    3'nos
                                                                                                                                                                                                                                                                                                                                                                                                         T-DNA
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/label= P35S
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                                                                                                                AAT39336 standard; DNA; 6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= g
/label= 3'g7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4336..5710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5711..6262
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6263..6496
                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                      /*tag= a
                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                    /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-402373/40.
                                                                                                                                                                                         Plasmid pTS174 used
                                                                                                                                                                                                                 pTS174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٦,
                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                            polyA_signal
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                                                                                                                                                                22-JAN-1997
                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                      AAT39336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter
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                                                                                                  AAT39336/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutate barnase gene for efficient construction of plant transformants, particularly male sterile plants free from any undesirable characters by specifically expressing the gene alone in anther -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 593
                                                                                                                                                                                                                                                                                          agtttaaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaacataa 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caggggcccgcgtaggcgatgccggcgacctcgccgtccacctcggcgacgagggga 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cggaagttgaccgtgcttgtctcgatgtagtggttgacgatggtgcagaccgccggcatg 833
                                                                      The invention relates to the generation of male sterile plants by the introduction of a mutant barnase gene (AA201095) for expression specifically in the anther of a plant. This sequence represents the coll/Agrobacterium shuttle vector plasmid pfS172 which contains the mutated barnase gene (AA291095) under control of the cauliflower mosaic virus 35S promoter. The vector also contains a region of the Agrobacterium T-DNA gene 7. The vector is used for transmitting the barnase gene to plants via an Agrobacterium tumefaciens host cell.
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         attgccgtagatgaaagactgagtgcgatattatgtgtaatacataaattgatgatatag
                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgtgcctccagggacttcagcaggtgggtgtagagcgtggagcccagtcccgttcgctgg
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                                                                                                                                                                                                                                        14.2%; Score 832.8; DB 21; Length 6539; 99.8%; Pred. No. 1.3e-130;
                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                    Sequence 6539 BP; 1755 A; 1578 C; 1519 G; 1687 T; 0 other;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                           The transformed plant is used in plant breeding.
                                                                                                                                                                                                                                                                 Mismatches
                                                Example 3; Page 23-27; 30pp; Japanese
                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                    Best Local Sim
Matches 834;
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                     174
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                                                                                                                                                                                                                                                                      AAT61394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter
                                                                                                                                              RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
3'UTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pTS174 (AAT39336) contains Bacillus barnase DNA under control of the stamen-specific PE1 promoter. Embryogenic callus from rice cv. Kochihibiti was transformed with pTS174 alone or with pTS88 (see also AAT3937), a plasmid contgo barstar DNA under control of a 35S promoter. With pTS174 alone, 1 male sterile line was recovered from 48 electroporation cuvettes. With both plasmids, 7 normal male sterile lines were recovered from 40 cuvettes. Barnase expression disturbed the function of stamen cells leading to male sterility. Constitutive expression of barnase in non-stamen tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6480 AGITTAAATATTATAGATAAAAAAAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 6421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attgccgtagatgaaagactgagtgcgatattatgtgtaatacataaattgatgatatag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 832.8; DB 17; Length 6548;
Pred. No. 1.3e-130;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6548 BP; 1757 A; 1578 C; 1523 G; 1690 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
      Page 33-37; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.2%;
99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.8 Matches 834; Conservative
Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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/*tag= d
/label= p35s
/note= "35s promoter region of cauliflower mosaic
virus"
                                                                                                                                                                                                                                                         /label- 3'nos
/note= "3' untranslated region contg. the poly-A
signal of Agrobacterium T-DNA nopaline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  '3' untranslated region contg. the poly-A signal of gene 7 of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase inhibitor - reduces the cultured cells response to stress and
                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= e
/label= Bar
/note= "phosphinothricin acetyltransferase"
                                                                                                                                          Transgenic plant; poly-(ADP-ribose) polymerase inhibitor; niacinamide; Agrobacterium; T-DNA; male sterile; barnase; ribonuclease; RNase; cereal; wheat; Triticum aestivum;
                                                                                                                                                                                                                                                                                                                                        /*tag= c
/label= pronoter region of rice El
complement (4336.5710)
                                                                                                                                                                                                                                 Location/Qualifiers
complement (2019..2288)
                                                                                                                                                                                                                                                                                          synthase gene"
complement (2289..2624)
                                                                                                                                                                                                                                                                                                                              complement (2625..4313)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 17-20; 25pp; English.
                                                                                                                                                                                         Chimeric Agrobacterium sp.;
Chimeric Oryza sativa;
Chimeric cauliflower mosaic virus.
                                                                                                                                                                                                                                                                                                                    /product= barnase
                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                AAT61394 standard; DNA; 6548
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/label= 3'
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                                                                                                                                                                       plasmid pTS172; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reduces metabolism
                                                                                                                         Plasmid pTS172.
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Plasmid pTS172 (AAT61394) contains the barnase coding sequence under control of the rice El gene stamen-specific promoter and a phosphnothrican acetyltransferase coding sequence under control of the cawy 35s promoter. Plasmid pTS172 and plasmid pTS772 (see also AAT61395) were used to transform wheat Spring variety Pavon calli via particle bombardment. Some calli were treated with the poly-(ADP-ribose) polymerase inhibitor niacinamide before, or before and after, bombardment. Healthy, male sterile plants were regenerated only from bombarded calli that were treated with niacinamide. This was believed to be due to more faithful expression characteristics of the integrated stamen-selective batnase gene in these calli and regenerated shoots. For plants transformed with pTS172, foreign DNA was stably incorporated in the wheat genome in 2-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413
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                                                                                                                                                                                                                                                                                                accggacgggcggtaccggcaggctgaagtccagctgccagaacccacgtcatgccag
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                                                                                                                                                                                                                                                                                                                                                                                                           174 atttattgatgcaagtttaaattcagaaatatttcaataactgattatatcagctggtac
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                                                                                                                                                                                                                                            Length 6548;
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                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                            DB 18;
                                                                                                                                                                                                                                                          Pred. No. 1.3e-130;
                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                           14.2%; Score 832.8; 99.8%; Pred. No. 1.3
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The invention relates to the generation of male sterile plants by the introduction of a mutant barnase gene (AAZ91095) for expression specifically in the anther of a plant. This sequence represents the E. coli/Agrobacterium shuttle vector plasmid pTS172 which contains the synthetic barnase gene (AAZ91094) under control of the cauliflower mosaic virus 35S promoter. The vector also contains a region of the Agrobacterium T-DNA gene 7. The vector is used for transmitting the barnase gene to plants via an Agrobacterium tumefaciens host cell. The transformed plant is used in plant breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutate barnase gene for efficient construction of plant transformants, particularly male sterile plants free from any undesirable characters by specifically expressing the gene alone in anther -
                                                                                                                                                                                                      Male sterile plant; mutant barnase gene; anther-specific expression; low fidelity PCR; primer; plant breeding; ss.
attgccgtagatgaaagactgagtgcgatattatgtgtaatacataaattgatgatatag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6548;
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                                                                                                                                                                            pTS172 containing synthetic barnase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 832.8; DB 21;
Pred. No. 1.3e-130;
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99.8%; Pred. No. 1.3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                           98JP-0220060
                                                                                                                                                                                                                                                                                                                               99WO-JP04167
                                                                                                                                                 (first entry)
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                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                           coli plasmid
                                                                                                                                                                                                                                                                        WO200008176-A1
                                                                                                                                                                                                                                                                                                                                                                                       (NISB ) JAPAN
                                                                                                                                                                                                                                                                                                                               03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                           04-AUG-1998;
                                                                                                                                               06-JUN-2000
                                                                                                                                                                                                                                                                                                     17-FEB-2000
                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                    Hamada K,
                                                                                                                    AAZ91096;
                                                                                            AAZ91096
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Best Local 3
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                                                                                                                                                                                                                                                                                      Plant promoter; root cell; root-specific expression; parasite resistance; nematode resistance; fungal resistance; water stress; salt stress;
              6241
                                                          6121
                                                                        473
                                                                                                                                                 5881
    353
                                                                                                                                                                                   833
                                                                                                                                                                                                                                                                                                                                                                                                      in roots, useful
accggacgggcggtaccggcaggctgaagtccagctgccagaaacccacgtcatgccag
                                                                  tgoatgogcacgetegggtegttggggcagecegatgacagegaceaegetettgaageee
                                                                                                             cggaagttgaccgtgcttgtctcgatgtagtggttgacgatggtgcagaccgccggcatg
                                                                                        tgtgcctccagggacttcagcaggtgggtgtagagcgtggagcccagtcccgtccgctgg
                                                                                                                                   Caggggcccgcgtaggcgatgccggcgactcgccgtccacctcggcgacgagccaggga
                                                                                                                                                         tagegetecegeagaegaegaggtegteegteeacteetgeggtteetgeggeteggta
                                                                                                                                                                                                    New constitutive plant promoter active specifically
                                                                                                                                                                                                                                                                          Nucleotide sequence of a plasmid PGKB5.
                                                                                                                                                                                                                                                                                                  sugar content; nitrogen transport; ss.
                                                                                                                                                                                                                                                                                                                                                                  (INRG ) INRA INST NAT RECH AGRONOMIQUE
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                                                                                                                                                                                                                                                                                                                                                                              Mollier P,
                                                                                                                                                                                                                                        AAF25320 standard;
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-102893/11
                                                                                                                                                                                                                                                                                                                      WO200100833-A1.
                                                                                                                                                                                                                                                                                                                                            23-JUN-2000;
                                                                                                                                                                                                                                                                30-APR-2001
                                                                                                                                                                                                                                                                                                                                                        25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                             Hoffmann B,
                                                                                                                                                                                                                                                                                                                                  04-JAN-2001
                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                     AAF25320
          6300
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The present sequence represents a plasmid PGKB5. The plasmid contains a plant promoter that directs expression of a selected sequence in root cells at all stages of development of a plant. The plant promoter is used to control expression of genes in a root-specific manner, especially genes that provide resistance to parasites, pests (nematodes or fungi), water and salt stress, or alter sugar content or nitrogen transport. Fragments of the promoter are useful as probes or primers to detect or amplify at least part of the promoter.
                                                                                                                                                                                                                                                                                                                                                 114 agtttaaatatttattgataaaataacaagtcaggtattatagtccaagcaaaaacataa 173
                                                                                                                                                                                                                                                                                                                             345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          645
        and
                                                                                                                                                                                                                                                                                                                                                                                                            6708 AGTTTAAATATTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctagcttagctcatcgggggatc----ctagaacgcgtgatctcagatctcggtga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTAGCTTAGCTCATCGGGGATCCATCGGATCCTAGACGCGTGAGATCAGATCTCGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcgcctcgtgcatgcgcacgctcgggtcgttgggcagcccgatgacagcgaccacgctct
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                                                                                                                                                                                                                                                                         Length 7599;
                                                                                                                                                                                                                 Sequence 7599 BP; 1972 A; 1938 C; 1937 G; 1752 T; 0 other;
                                                                                                                                                                                                                                                                                                       Indels
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                                            9; 92pp; French.
   expression of
                plants
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                transgenic
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nes 828; Conserv
                                         Disclosure; Flg
controlling
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Query Match
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       ccggcatgtccgcctcggtggcacggcggatgtcggccgggcgtcgttctgggtccattg 885
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                                                                                                                                                                                                                                                                                                                                                                                      region containing polyA signal of
Agrobacterium T-DNA nopaline synthase gene"
                                                                                                                                                                                                                                                            coding
                                                                                                                                                                                                                                                                                                                                                     coding
                                                                                                                                                                                                                                                                                                                         35S promoter"
                                                                                                                               Plasmid pVE136; male sterile; barnase; ribonuclease; barstar;
transgenic plant; maize; corn; Zea mays; ds.
                                                                                                                                                                                                                                                            /note= "Bacillus amyloliquefaciens barnase
                                                                                                                                                                                                                                                                                                                                                    /note= "phosphinothricin acetyltransferase
                                                                                                                                                                                                                                                                                             /note= "maize CA55 gene promoter"
1956..2788
                                                                                                                                                                                                                                                                                                                         'note- "cauliflower mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                        pUC19"
                                                                                                                                                                                            /note= "polylinker of pUC19" complement (28..403)
                                                                                                                                                                                                                                                                                                                                                                                     'note= "region containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cornelissen M, Michiels F;
                                                                                                                  Plasmid pvE136 (EcoRI-HindIII fragment).
                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= h
/label= pUC19
/note= "polylinker of
                                                                                                                                                                                                                                                                         complement (740..1918)
                                                                                                                                                                   Location/Qualifiers
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                                                                          BP.
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/label= Barnase
                                                                                                                                                                                                                                                                  region"
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/*tag= a
/label= puc19
                                                                                                                                                                                                            /*tag= b
/label= 3'nos
                                                                                                                                                                                                                                                                                  *tag= d
label= PCA55
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/label= 3'nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENETIC SYSTEMS
                                                                         AAT39338 standard; DNA; 3658
                                                                                                                                                                                                                                                                                                                  /label- P35S
                                                                                                                                                                                                                                                                                                                                             /label- bar
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                                                                                                      entry)
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                                                                                                      (first
                                       5928 ATCCGATTT 5920
                          ttcttcttt 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PLBZ ) PLANT
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                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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                                                                                                                                                                                                     polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-1995;
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                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctgaatttctgaagcctgatgtatagttaatatccgcttcacgccatgttcgtccgcttt 3169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 ggattcaatcttaagaaactttattgccaaatgtttgaacgatctgcttcggatcctcta 300
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                                                                                                                                                                                                                           The ECORI-HindIII fragment (AAT39338) of plasmid pvE136 contains a Bacillus barnase (ribonuclease) gene under control of the PCA55 promoter. Embryogenic callus from maize was transformed with pVE136 and pTS88 (see also AAT39337), a pGEM2-derived plasmid contg. barstar DNA under control of a 355 promoter. Maize plants contg. both P35S-barstar-3'g7 and the PCA55-barnase-3'nos chimeric genes were male sterile. Foreign genes such as barnase can be placed under control of a stamen-specific promoter to produce male sterile plants; constitutive expression of barstar counteracts any low level expression of barnase in other tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggattcaatcttaagaaactttattgccaaatgtttgaacgatctgcttcggatcctcta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gagccggaaagtgaaattgaccgatcagagtttgaagaaaaaatttattacacactttatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 741.8; DB 17;
Pred. No. 1.9e-115;
0; Mismatches 2;
                                                                                                                                                                               Example 2; Page 40-42; 56pp; English.
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99.7%;
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Matches 743; Conservative
1996-402373/40.
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/note= "3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA nopaline synthase gene."
                                                                                                                          Maintainer gene; sterile; sterility; homogenous population; hybrid; seed; fertility restorer gene; pollen lethality gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                35S3" promoter sequence derived from cauliflower mosaic virus isolate CabbB-JI."
                                                                                                            Restriction fragment of construct carrying plant maintainer gene.
                                                                                                                                                                                                                                                                        Zea
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                                                                                                                                                                                                                                                                   /note= "Promoter region of the Zm 13 gene of
                                                                                                                                                                                                                                                                                                                         /note- "Coding region of the barstar gene of Bacillus amyloliquefaciens." complement (2555.3099)
                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Coding region of the phoshinothricin
                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                 /notes "Coding region of the barnase gene
Bacillus amyloliquefaciens."
complement (738..1944)
                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                            /note= "Promoter region of the TA29
                                                                                                                                                                                                                                                                                                                                                                     Nicotiana tabacum
                                                                                                                                                                                                                                                                                  complement (1945..2281)
                                                                                                                                                                                                                                                                                                 /label 3' nos.
complement (2282..2554)
                                                                                                                                                              Location/Qualifiers
complement (18..401)
                    tgttgataaccggtaccatggtagc 3374
                            Barnase.
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/label= Barstar.
                                                                                                                                                                                  3' nos
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                                                                  AAQ53889 standard; DNA; 4808
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/label= 35S3
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/label~ 3'
/note~ "3'
                                                                                                (first entry)
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/label= 3'
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                                                                                               27-JUN-1994
                                                                                                                                                                   misc_signal
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                                                                                                                                                                                                                                                                                  misc_signal
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                                                                                 AAQ53889;
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    1810 attacatgcttaacgtaattcaacagaaattatatgataatcatcgcaagaccggcaaca 2869
    1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 1811 | 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
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                                                                                                                                                                                                                                                        Maintainer gene for maintenance of male-sterile plants -comprises fertility-restorer gene and pollen-lethality gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4808 BP; 1370 A; 1064 C; 1037 G; 1333 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and comprises the maintainer gene described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.4%; Score 727.8; DB 15; 99.2%; Pred. No. 4.4e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                        English.
(PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 73-75; 87pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.29
Watches 743; Conservative
                                                                                          Leemans J, Williams
                                                                                                                                                                           WPI; 1994-007552/01.
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06-JUN-1995;
                   06-JUN-1994;
                                               Krebbers E,
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                                C1; C1-S; transgenic plant; male sterility; colour-linked restorer;
anthocyanin; aleurone; B-peru; bar; barstar; bar*; ds.
     ggagcgacgtctgcaaggttcccttttgatgccacccagccgagggcttgtggcttctgat
                   ggagcgacgtctgcaaggttcccttttgatgccacccagcccagggcttgtgcttctgat
                                                                                                                                                                                                                                                                                                                    Mosaic Virus"
                                                                                                                                                                                                                                      /note= "3' regulatory sequence contg. the polyadenylation signal of the nopaline synthase gene of Agrobacterium T-DNA" complement (318.869)
                                                                                                                                                                                                                                                                                                                                                                                                                      3' regulatory sequence contg. the polyadenylation signla of the nopaline synthase gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                               of TA29 gene of Nicotiana
                                                                                                                                                                                                                                                                                                                                                                                    ō
                                                                                                                                                                                                                                                                                                                                                                                   /note= "coding region of barstar gene
                                                                                                                                                         P35S-bar-3'nos and PTA29-barstar-3'nos
                                                                                                                                                                                                                                                                                /note= "coding region of bar gene of Streptomyces hygroscopicus"
                                                                                                                                                                                                                                                                                                                    promoter of Cauliflower
                                                                                                                                                                                                                                                                                                                                                                                           Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= h
/label= pUC19
/note= "pUC19 derived sequence"
                                                             aacgtgttgataaccggtaccatggtagc 3374
                                                                                                                                                                                                                                                                                                                           complement (1740..2284)
                                                                    Streptomyces h complement (870..1702)
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complement (39..317)
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tabacum"
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/label~ barstar
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/label= 3'nos
                                                                                                              AAT08976 standard; DNA; 4896
                                                                                                                                                                                                                                                                                                           /label= P35S
                                                                                                                                                                                                                                                                                                                   /note= "35S
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2880..4986
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/label= 3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           easier
                                                                                                                                                                                                                                                          Transgenic plants contg. male sterility and colour-linked restorer genotypes - used for prodn. of male sterile seeds identifiable from their colour, also new truncated anthocyanin regulatory genes and aleurone specific promoters
                                                                                                                                                                                                                                                                                                                                                                                                                                             Shortened forms of anthocyanin (An) regulatory genes (ARG) are easi to manipulate than the complete gene and still provide An prodn. The Cl gene (and the Cl-S gene) can be considerably shortened while still retaining, under appropriate conditions, its capability of conditioning anthocyanin prodn. in the aleurone of seeds of cereal plants such as corn. A pref. shortened Cl gene is comprised in partole9 (see AAT08975). The full Cl gene sequence is Atrucated B-peru gene (presumed sequence - AAT08977) may also be used.

Plasmids pTS256 (AAT08976) and pTS200 (AAT17246) were used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2671 CAGGATTCAATCTTAAGAAACTTTATTGCCAAATGTTTGAACGATCTGCTTGGATCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 construction of vectors comprising the Cl and B-peru genes as well as male-sterility gene and a selectable marker gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4896 BP; 1252 A; 1146 C; 1186 G; 1312 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.1%; Score 712; DB 17;
llarity 76.7%; Pred. No. 1.9e-110;
Conservative 0; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 68-71; 104pp; English.
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                                                                                                       GENETIC SYSTEMS
                                                  94US-0254776
95WO-EP02157
                                                                                                                                                            Leemans J,
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Best Local Similarity
Matches 987; Conserv
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                                                                                                     3168 tttgcccgggagtttgccttccctgtttgagaagatgtctccgccgatgctttccccgg
                          3228 agogacgictgcaaggitcccitttgatgccacccagccgagggcttgtgcttctgatti
                                                ODDITE:
                                                                                             3348 cgigitgalaaccggtaccaiggtagctaatttctttaagtaaaaactttgaittgagtg
                                                                                                                                                                           ggaaaaagtaccaaaattttgtctcaccctgatttcagttatggaaattacattatgaag
                                                                                                                                                                                                             gctttaattcgagtaggatgtatatattagtacataaaaaatcatgtttgaatcatctt
                                                                                                                                                                                                                                                                                             cataaagtgacaagtcaattgtcccttcttgtttggcactatattcaatctgttaatgca
                                                                                                                                                                                                                                                                                                                        Cl gene; maize; male-sterile corn line; anthocyanin production;
pTS256; ds.
GCCTCCATTCCAAAACGAGCGGGTACTCCACCCATCCGGT-
                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of plasmid pTS256.
                                                                                                                                                                                                                                                                                                                                         3888 mattatccagttatacttagctagat 3913
                                                                                                                                                                                                                                                                                                                                                   DNA; 4896
                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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2450
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The present sequence represents the nucleotide sequence of plasmid pr5256. It is used in the course of the invention. The specification describes a process for maintaining a male-sterile corn line, using male sterile parent plants lacking a functional gene for anthocyanin production, and a maintainer corn line comprising male fertile parent production, and a maintainer corn line comprising male fertile parent regulatory protein gene. By using the anthocyanin gene, the colour of the male-sterile plants will differ from that of the male fertile plants. This will enable the seeds harvested from the plants to be easily separated into those that will grow into male-fertile plants and those that will grow into male-sterile plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2628 cggaattcgagctcggtacccggggatcttcccgatctagtaacatagatgacaccgcgc 2687
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                                                                                                                                                                   Process for maintaining a male-sterile corn line – using male
sterile plants lacking functional regulatory gene for anthocyanin
production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2912 CAGAATTCGAGCTCGGTACCCGGGGATCTTCCCGATCTAGTAACATGACACGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4896 BP; 1251 A; 1147 C; 1186 G; 1312 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 708.8; DB 20;
Pred. No. 6.6e-110;
0; Mismatches 187;
                                                                                                                                                                                                                      Example 2; Columns 31-36; 35pp; English.
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                                                                                                                  Williams
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                                                                                 (PLBZ ) PLANT GENETIC SYSTEMS
                95US-0485139
                                            95US-0485139.
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76.6%;
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Best Local Similarity 76.6
Matches 985; Conservative
                                                                                                                 Leemans J,
                                                                                                                                        WPI; 1999-204053/17
                                         07-JUN-1995;
06-JUN-1994;
             07-JUN-1995;
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2502 GAAGCACACTCTCGGCGCCAIT-----TICAGTCAGCTGCTTGCTTTGTTCAAACT 3108 gicigaailicigaagceigaigiatagilaaataleegeelteaegeeatgilegieegei

3048 aaaggtotgataatggtoogttgttttgtaaatcagocagtogottgagtaaagaatoog

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> US5880331-A 09-MAR-1999

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                                                                                                             gcttgattcaaaaactgatttaatttacattgctaaatgtgcatacttcgagcctatgtc
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3168 tttgcccgggagtttgccttccctgtttgagaagatgtctccgccgatgcttttccccgg
                                                                    2066 GGAAAAAGTACCAAAATTTTGTCTCACCCTGATTTCAGTTATGGAAATTACATTATGGAG
                                                      tgtaatgtaattatcaggtagcttatgatatgtctgaagataatccgcaaccccgtcaaa
        -----CAGACAATCCCATAAAGCGTCCAGGTTTTCACCGTAGTATTCCGGAAG
                          3228 agcgacgictgcaaggitcccitttgatgccacccagccgagggcttgtgcttctgatti
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Sequence 1 Sequence 4 Sequence 4 Sequence 5 Sequence 5 Sequence 5 Sequence 5 Sequence 5 Sequence 6 Sequence 6

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LOCATION: Complement((2659)..(3031))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3'nos)
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LOCATION: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of corres information: of Agrobacterium T-DNA (3'97)
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LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco
OTHER INFORMATION: Arabidopsis (Pssu)
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OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
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LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
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TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NMSCOR
CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
US-08-351-413-17

US-09-025-583-17

US-08-04-121-4

US-08-318-772A-1

US-08-478-015-4

US-08-478-015-4

US-08-4889-4

US-08-189-2

US-08-189-2

US-08-104-073-2

US-08-351-413-3

US-09-025-583-3

US-08-08-104-073-5

PCT-US91-06234A-1

US-08-817-188-4

US-08-817-188-4

US-08-817-188-10

US-08-817-188-10

US-08-817-188-10

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US-08-844-4678-10
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- 2000 Compugen Ltd.
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    nucleic search, using sw model

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                gene
                             NAME/KEY: misc_feature

LOCATION: (4924)..(5216)

OTHER INFORMATION: promoter of nopaline synthase gene of
OTHER INFORMATION: Agrobacterium T-DNA (Phos)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5217)..(5489)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amiloliquefaciens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5490)..(5765)
OTHER INFORMATION: region containing polyadenylation signerammer.
OTHER INFORMATION: region containing polyadenylation signerammer.
                                               of
                                                                               Bacillus
                                                                                                                                               T-DNA
               TA29
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NAME/KEY: misc_feature
LOCATION: Complement((5840)..(5864))
OTHER INFORMATION: left border of Agrobacterium
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LOCATION: Complement((3368)..(4877))
OTHER INFORMATION: promoter of stamen-specific
OTHER INFORMATION: tabacum (PTA29)
FEATURE:
                                                                                                                                                                       Score 5843.4; Pred. No. 0; 0; Mismatches
                                                                                                                                                                      Match 99.6%;
Local Similarity 99.9%;
Nes 5858; Conservative 0
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US-08-894-440-4
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Best Local S:
Matches 5858
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FION: GENETIC TRANSFORMATION USING A PARP INHIBITOR

FION: 2121-0127P

CATION NUMBER: US/08/817,188

DATE: 1997-05-15

DATE: 1996-07-31

WITON NUMBER: PP 95401844.6

DATE: 1995-08-04
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OTHER INFORMATION: Description of Artificial Sequence: T-DNA of FEATURE:
NAME/KEY: misc_feature
LCCATION: Complement((1)..(25))
OTHER INFORMATION: T-DNA right border (RB)
FEATURE:
NAME/KEY: misc_feature
LCCATION: Complement((1)..(330))
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacter OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacter OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacter OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacter OTHER INFORMATION: bar: region coding for phosphinotricin acetyl OTHER INFORMATION: bar: region coding for phosphinotricin acetyl OTHER INFORMATION: bar: region coding for phosphinotricin acetyl OTHER INFORMATION: promoter region of Rubisco small subunit gene FEATURE:
NAME/KEY: misc_feature
LCCATION: Complement((3639)..(3031).)
OTHER INFORMATION: polyadenylation signal of the nopaline synthas OTHER INFORMATION: gene of Agrobacterium T-DNA
FEATURE:
NAME/KEY: misc_feature
COTHER INFORMATION: polyadenylation signal of the nopaline synthas OTHER INFORMATION: barnase: region coding for barnase
FEATURE:
NAME/KEY: misc_feature
LCCATION: Complement((3032)..(3367))
OTHER INFORMATION: barnase: region coding for barnase
FEATURE:
NAME/KEY: misc_feature
LCCATION: Complement((4922)..(4946))
OTHER INFORMATION: Labacum
FEATURE:
NAME/KEY: misc_feature
NAME/
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region containing the of gene 7 of Agrobacterium
           aatccctaatataatcgcgacggatccccgggaattccggggaagcttagatccatgcag
                                                                                              ataatctatgtatatggttagaaaaagtaaacaattaatatagccggctatttgtgtaaa
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LOCATION: (2765)..(3058)
OTHER INFORMATION: 3' untranslated region of
OTHER INFORMATION: containing polyadenylation
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OTHER INFORMATION: RB: right border sequence
OTHER INFORMATION: pTib6S3
                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USI
FILE REFERENCE: 2121-0127P
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT FILING DATE: 1997-05-15
EARLIER FILING DATE: 1996-07-31
EARLIER FILING DATE: 1996-07-31
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VOR: 5
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (84)..(296)
OTHER INFORMATION: 3' 97: 3' untranslated
OTHER INFORMATION: polyadenylation signal
OTHER INFORMATION: T-DNA
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LOCATION: (3059)..(5056)
OTHER INFORMATION: uida:
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NAME/KEY: misc_feature
LOCATION: (84)..(296)
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NAME/KEY: misc_feature
LOCATION: (318)..(869)
OTHER INFORMATION: bar:
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LOCATION: (830)..(2760
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NAME/KEY: misc_feature
LOCATION: (5077)..(5078)
OTHER INFORMATION: region with unknown sequence
OTHER INFORMATION: nucleotides)
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LOCATION: (5476)..(5479)
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US-08-817-188-5
                                                                                   left border sequence of
            region corresponding
ST-LS1 gene
                                                     region
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Pred. No. 0;
0; Mismatches
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LOCATION: (4483)...(4671)
OTHER INFORMATION: 1V2: region colorther INFORMATION: 1V2: region colorther INFORMATION: the ST-LS1 gene FEATURE:
NAME/KEY: misc_feature
LOCATION: (5067)...(5502)
OTHER INFORMATION: P3SS: 35S promc PAETURE:
NAME/KEY: misc_feature
LOCATION: (5533)..(5560)
OTHER INFORMATION: LB: left border OTHER INFORMATION: pTIB6S3
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5058)..(5059)
OTHER INFORMATION: region with unk OTHER INFORMATION: nucleotides)
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NAME/KEY: promoter LOCATION: 1139.11683 O'THER INFORMATION: /function= sequence derived from OTHER INFORMATION: /function= specific promoter of Nicotiana tabacum"
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                                                                                                                                       APPLICANT: Michiels, Frank
APPLICANT: Morioka, Sinji
APPLICANT: Morioka, Sinji
APPLICANT: Scheirlinck, Trees
APPLICANT: Komari, Tosihiko
TITLE OF INVENTION: Stamen-specific Promoters from Rice
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1..395
OTHER INFORMATION: /product= "pUC18 derived sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 08 FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOWALONY, KALHAETINE M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.93USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                      ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5639948west Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/104,072B
FILING DATE: 05-AUG-1993
CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 10-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91402590.3
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91400318.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 9200272
FILING DATE: 06-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91403352.7
FILING DATE: 10-DEC-1991
                                                                                            Sequence 9, Application US/08104072B Patent No. 5639948
                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
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 LENGTH: 5620 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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LOCATION: 396..802
OTHER INFORMATION: /s
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STRANDEDNESS: double
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3808 atcatgtttgaatcatctttcataaagtgacaagtcaattgtcccttcttgtttggcact 3867
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APPLICANT: Leemans, Jan
TITLE OF INVENTION: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08351413
Patent No. 5750867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
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US-08-351-413-3
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                                                                                                                                                                                                                           Score 1270.4; DB 1; Length 5620;
Pred. No. 3e-268;
0; Mismatches 11; Indels 4;
                                                                                                                                                                                                                                             11; Indels
                                                                     NAME/KEY: CDS
LOCATION: 2557.3068
COTHER INFORMATION: /Product= "CDS of phosphinotricin OTHER INFORMATION: acetyltransferase gene"
NAME/KEY: polyA_site
LOCATION: 3069.3356
OTHER INFORMATION: /standard_name= "Agrobacterium OTHER INFORMATION: T-DNA nopaline synthase gene"
                                                                                                                                                                   ; NAME/KEY: misc_feature
; LOCATION: 3357..5620
;; OTHER INFORMATION: /product= "pUC18-derived sequence"
US-08-104-0728-9
                          NAME/KEY: promoter
LCCATION: 1684..2515
OTHER INFORMATION: /standard_name= "3553 promoter
OTHER INFORMATION: sequence from Cauliflower mosalc
FEATURE:
            barnase gene'
            oţ
           "CDS
LOCATION: 803.1138
OTHER INFORMATION: /product=
                                                                                                                                                                                                                          Query Match
21.7%;
Best Local Similarity 98.9%;
Matches 1291; Conservative
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Best Local Similarity 98.9
Matches 1291; Conservative
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OTHER INFORMATION: /label= 3'nos
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
TIDNA nopaline synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (396..802)

RMATION: /label= 3'nos

RMATION: /note="3' regulatory sequence containing the

RMATION: polyadenylation site derived from the nopaline

RMATION: synthase gene from Agrobacterium T-DNA"
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LOCATION: 2517..3068
COTHER INFORMATION: /label- bar
OTHER INFORMATION: /note= "coding sequence of phosphinotricin
OTHER INFORMATION: acetyltransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (803..1138)
RMATION: /lobe- barnase RMATION: /note- "coding region of the barnase gene RMATION: Bacillus amyloliquefaciens"
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NAME/KEY:
LOCATION: 1684..2516
OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /note= ""35S3" promoter sequence derived f
OTHER INFORMATION: /note= ""35S3" promoter sequence derived f
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NAME/KEY:
LOCATION: complement (1139..1683)
COTHER INFORMATION: /label= TA29
OTHER INFORMATION: /note= "sequence derived from tOTHER INFORMATION: promoter of Nicotiana tabacum"
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OTHER INFORMATION: /label- pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
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/note= "pUC18 derived sequence"
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                                                                                                                                                                                                                                                                                                                                                ORGANISM: plasmid pVE108 (replicable in
                                                NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                TELEX: 248345
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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LOCATION: complement
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FRAUKE:
NAME/KEY:
-LOCATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 1,,395
OTHER INFORMATION:
OTHER INFORMATION:
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ORIGINAL SOURCE
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NAME/KEY: -
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DB 1; Length 5620;

Score 1270.4;

21.78;

Query Match

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           Gaps
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                                        3088 togottgagtaaagaatcoggtotgaatttotgaagootgatgtatagttaatatoogot
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           Indels
          11;
 Pred. No. 3e-268;
0; Mismatches 1
98.98;
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NAME/KEY: -
-LOCATION: 3069..3356
OTHER INFORMATION: /Label-3'nos
OTHER INFORMATION: polyadenylatic
OTHER INFORMATION: polyadenylatic
OTHER INFORMATION: T-DNA nopaline
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1684..2516
                                                                                          NAME/KEY:
LOCATION: Complement
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
LOCATION:
COTHER INFORMATION:
OTHER INFORMATION:
                    LOCATION: 1..395
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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Sequence 3, Application US/09025583
Patent No. 597433
GENERAL INFORMATION:
APPLICANT: Williams, Mark
TITLE OF INVENTION: Maintenance of male-sterile plants
TITLE OF INVENTION: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatchouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                   3868 ataticaatctgttaatgcaaattatccagttatacttagctagat 3913
                                                                                                                                                                                                                                                                                     1638 ATATTCAATCTGTTAATGCAAATTATCCAGTTATGTTAGCTAGAT 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FYTING DAME: US/09/025;583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: plasmid pVE108 (replicable in E.coli)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIDR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTONNEY/AGENT INFORMATION:
NAME: SVENSSON, LECONATON:
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMOUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
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RMATION: /label= 3'nos

RMATION: /note= "3' regulatory sequence containing the RMATION: polyadenylation site derived from the nopaline RMATION: synthase gene from Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA nopaline synthase gene"
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                                                                                                                                                                                                                                                                                                                                                                                   complement (1139..1683)
RMATION: /label= TA29
RMATION: /note= "sequence derived from tapetum specific RMATION: promoter of Nicotiana tabacum"
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OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /note= ""35S3" promoter sequence derived from OTHER INFORMATION: cauliflower mosaic virus isolate Cabbb-JI"
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NAME/KEY:
LOCATION: 2517..3068
OTHER INFORMATION: /label= bar
OTHER INFORMATION: /note= "coding sequence of phosphinotricin
OTHER INFORMATION: acetyltransferase gene"
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Best Local Similarity 98.9%; Pred. No. 3e-268;
Matches 1291; Conservative 0; Mismatches 11; Indels 4;
                                                                                                                                                                                                                                                                       /label= barnase
/note= "coding region of the barnase
Bacillus amyloliquefaciens"
/label= pUC18
/note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : NAME/KEY: -
. LOCATION: 3357..5620
. O'THER INFORMATION: /label= pucl8
. O'THER INFORMATION: /note= "pucl8 derived sequence"
US-09-025-583-3
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                       FEATURE
                                                                                                                                                                  tctgcttcggatcctctagag----ccggaaagtgaaattgaccgatcagagtttgaaga 2967
                          tcgcttgagtaaagaatccggtctgaatttctgaagcctgatgtatagttaatatccgct 3147
                                                                                                           tcacgccatgttcgtccgcttttgcccgggagtttgccttccctgtttgagaagatgtct 3207
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OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA noppline synthase gene "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
CORRESPONDENCE ADDRESS: 5
CORRESPONDENCE ADDRESS: 5
CORRESPONDENCE AMSON Bldg., Washington & Prince Sts.
CITY: Alexandria
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STRATE: Viriginia
COUNTRY: United States
ZIR: 22313-1404
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/064,121
FILING DATE: 24-MAY-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= PTA29
/note= "Promoter from the TA29
tabacum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90403332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36,113
SR: 010830-043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Crane-Feury, Sharon E REGISTRATION NUMBER: 36,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: fragment of pTTM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1287 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 99.7
Matches 1283; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
US-08-064-121-3
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OTHER INFORMATION:
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NAME/KEY:
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NAME/KEY:
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; Sequence 3, Application US/08064121
; Patent No. 5641664

US-08-064-121-3/c

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MOLECULE TYPE:
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/label- PTA29
/note= "Promoter from the TA29 gene of Nicotiana tabacum"
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                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,015
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9040332.1
FILING APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING APPLICATION NUMBER: BP 91401888.2
FILING APPLICATION NUMBER: US 08/064,121
FILING NUMBER: US 08/064,121
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MONOCOTYLEDONOUS PLANTS
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US-08-478-015-3/c
Sequence 3, Application US/08478015;
Patent No. 5712.135
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APPLICANT: D'HALLUIN, Kathleen
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR
TITLE OF INVENTION: MONOCOTYLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: fragment of pTTM8
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P.O. Box 1404
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 39,3
REFERENCE/DOCKET NUMBER:
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ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Do
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STRANDEDNESS: double
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OTHER INFORMATION:
OTHER INFORMATION:
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CITY: Alexandria
STATE: Virginia
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                                                           aatctgagggtaacattaaggtttcatgtattaatttgttgcaaacatggacttagtgtg
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STREET: George Mason Bldg., Washington & Prince
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUINS, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURES: STEM PC COMPATIBLE
OPERATURES: SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,975
FILING DATE: 07-UN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,121
APPLICATION NUMBER: US 08/064,121
FILING DATE: 24-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: EP 9040332.1 FILING DATE: 24-MAY-1993
APPLICATION NUMBER: EP 9040332.1 FILING DATE: 23-NOV-1990
PRIOR APPLICATION DATA: APPLICATION NUMBER: EP 91401888.2 ATTORNEY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: D'HALLUIN, Kathleen
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FILING DATE: 08-JUL-1991
ATTORNEY/AGENT INFORMATION:
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US-08-475-975-3/c
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                                          barnase gene'
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                        OTHER INFORMATION: /label= barnase
OTHER INFORMATION: /note= "coding sequence of
                                                                                                                                                                                       Score 1269; DB 1;
Pred. No. 3.1e-268;
0; Mismatches 0;
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                                                                                                                                                                                                      Best Local Similarity 99.7
Matches 1283; Conservative
                                                                   NAME/KEY:

LOCATION: 882..1287

OTHER INFORMATION:

OTHER INFORMATION:

OTHER INFORMATION:

US-08-478-015-3
                                                                                   882..1287
NAME/KEY:
LOCATION:
                                                                                                                                                                                          Query Match
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ADDRESSEE: Burns, Doane,
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US-09-084-889-3/C
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Pred. No. 3.1e-268;
0; Mismatches 0; Indels 4
                                                                                                                                                                     FEATURE:
NAME/KEY: -
LOCATION: 546..881
OTHER INFORMATION: /label- barnase
OTHER INFORMATION: /note- "coding sequence of barnase
                                                                                                                                                                                                                             NAME/KEY: -
LOCATION: 882.,1287
COTHER INFORMATION: /Label= 3'nos
OTHER INFORMATION: /note= "3' reg
OTHER INFORMATION: Polyadenjlatic
OTHER INFORMATION: T-DNA nopalatic
                                                                                                         pTTM8
                                                                                                                                                                tabacum"
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1287 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                   21.6%;
99.7%;
                                                                                                      ORGANISM: fragment of
                                                                                                                                                                                                                                                                                                                                    Matches 1283; Conservative
                                                                                                                       NAME/KEY:
LOCATION:
LOCATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                          linear
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                                                     TOPOLOGY: 11ne
MOLECULE TYPE: D
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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George Mason Bldg., Washington & Prince
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Patent No. 6074877
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: D'HALLIN, Kathleen
APPLICANT: GOBEL, Blke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aaattatccagttatacttagctagat 3913
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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3106

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aatctgagggtaacattaaggtttcatgtattaatttgttgcaaacatggacttagtgtg 3586
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US-08-817-188-2/c
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/note= "3' regulatory sequence containing the
polyadenylation site derived from Agrobacterium
T-DNA nopaline synthase gene "
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                                                                                                                                                                                                                                                                                                                                                                                          /label= PTA29
/note= "Promoter from the TA29
tabacum"
SUFTWARE: Patentin Release #1.0, Version #1.25
LICHRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 546..881
OTHER INFORMATION: /label- barnase
OTHER INFORMATION: /note- "coding sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 21.6%; Score 1269; DB 3;
Best Local Similarity 99.7%; Pred. No. 3.1e-268;
Matches 1283; Conservative 0; Mismatches 0;
                                                                                                                                                 NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REGISTRENCE/DOCKET NUMBER: 010830-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAR: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                APPLICATION NUMBER: US/09/084,889 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,121
                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                              LENGTH: 1287 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                             ORGANISM: fragment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 882.1287
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
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NAME/KEY:
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OTHER INFORMATION: Description of Artificial Sequence: plasmid PTS172

NAME/KEY: misc_feature

LOCATION: Complement((2019)..(2288))

OTHER INFORMATION: 3 nos: 3' untranslated region containing the OTHER INFORMATION: 9 nos: 3' untranslated region containing the OTHER INFORMATION: 9 nos: 3' untranslated region containing the OTHER INFORMATION: polyadenylation signal of the nopaline synthase of THER INFORMATION: polyadenylation signal of the nopaline synthase CTHER INFORMATION: per of Agrobacterium T-DNA.

NAME/KEY: misc_feature

LOCATION: Complement((2025)..(4313))

OTHER INFORMATION: PEl: promoter region of El gene of rice FEATURE:

NAME/KEY: misc_feature

LOCATION: Complement((2010))

OTHER INFORMATION: Virus

FEATURE:

NAME/KEY: misc_feature

LOCATION: Complement((5711)..(6262))

OTHER INFORMATION: Virus

FEATURE:

NAME/KEY: misc_feature

LOCATION: Complement((5711)..(6262))

OTHER INFORMATION: Dar: region coding for phosphinotricin of FEATURE:

NAME/KEY: misc_feature

LOCATION: Complement((5711)..(6262))

OTHER INFORMATION: dectyltransferase

NAME/KEY: misc_feature

LOCATION: Complement((5711)..(6262))

OTHER INFORMATION: 3'97: 3' untranslated region containing the CATION: CATION: PEATURE

NAME/KEY: misc_feature

LOCATION: (5659)..(6456)

OTHER INFORMATION: 3'97: 3' untranslated region containing the OTHER INFORMATION: 1-DNA

OTHER INFORMATION: 7-DNA

OTHER INFORMATION: 7-DNA
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                                                        APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-01279
CURRENT APPLICATION WUMBR: US/08/817,188
CURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBRE: PCT/EP96/03366
EARLIER FILING DATE: 1996-07-31
EARLIER FILING DATE: 1996-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATCHIN VOL. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,
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Pred. No. 1.4e-172;
0; Mismatches 2;
Sequence 2, Application US/08817188
Patent No. 6074876
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.2%;
99.8%;
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Best Local Similarity 99.8
Matches 834; Conservative
                                                                                                                                                                                                                                                                                                 LENGTH: 6548
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                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: (1)..(2003)
OTHER INFORMATION: pUC19 derived vector sequences (vector)
FEATURE:
ctagettageteategggggatectagaacgegtgateteagateteggtgaegggeagg
                                                                                                               accggacgggcggtaccggcaggctgaagtccagctgccagaaaccacgtcatgccag
                                                                                                                                                                                                                                  tgtgcctccagggacttcagcaggtgggtgtagagcgtggagcccagtcccgtccgctgg
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of Agrobacterium
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Franche.

Franche.

LOCATION: Complement((2019)..(2283))

OTHER INFORMATION: 3' nos: region containing polyadenylat OTHER INFORMATION: 0f nopaline synthase gene of Agrobacte FEATURE:

NAME/KEY: misc_feature

LOCATION: Complement((2284)..(2624))

OTHER INFORMATION: region coding for barnase of Bacillus OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/0889440
Patent No. 602546
GENERAL INFORMATION:
APPLICAME: PLANT GENERAL SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
TILE REPERENCE: NMSCOR
CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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LENGTH: 6548
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OTHER INFORMATION: Description of Artificial Sequence: ECORI-HindIII OTHER INFORMATION: fragment of pVE136
                                                                                cggaagttgaccgtgcttgtctcgatgtagtggttgacgatggtgcagaccgccggcatg
                                             5820 CGGAAGTTGACCGTGCTTGTCTCGATGTAGTGGTTGACGATGGTGCAGACCGCCGGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: Complement((28)..(403))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3'nos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (3341)..(3623)
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3'nos)
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OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
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OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                  APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REPERENCE: NMSCOR
CURRENT APPLICATION UNBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 3658
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LOCATION: (1956)..(2788)
OTHER INFORMATION: 35S promoter of Cauliflower Mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.6%; Score 741.8; DB 3; 99.7%; Pred. No. 8.2e-153; tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: Complement((740)..(1918))
OTHER INFORMATION: promoter of CA55 gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)...(26)
OTHER INFORMATION: polylinker of puc19
                                                                                                                                                                                                             ; Sequence 3, Application US/08894440
; Patent No. 6025546
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LOCATION: (3624)..(3658)
OTHER INFORMATION: polylinker of
.08-894-440-3
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Matches 743; Conservative
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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US-08-894-440-3
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NAME/KEY: misc_feature
LOCATION: Complement((2625)..(4313))
COTHER INFORMATION: (PEL)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4336)..(5710)
OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5711)..(6262)
OTHER INFORMATION: region coding for phosphinothricin acetyl
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5713)..(6495)
OTHER INFORMATION: region coding for phosphinothricin acetyl
FEATURE:
LOCATION: (6263)..(6496)
OTHER INFORMATION: region containing polyadenylation signal fo gene
COTHER INFORMATION: region containing polyadenylation signal fo gene
COTHER INFORMATION: region containing polyadenylation signal fo gene
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Pred. No. 3.1e-172;
0; Mismatches 3;
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Matches 833; Conservative
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                                                                                                                                                                                                                                                                                           aggictgataatggiccgitgittigtaaatcagccagicgcitgagtaaagaatccggt 3109
                                                                                                                                                                                                                                                                                                                                   ctgaatttctgaagcctgatgtatagttaatatccgcttcacgccatgttcgtccgcttt 3169

    1870 ggattcaatcttaagaaactttattgccaaatgtttgaacgatctgcttcggatcctcta 2925
    241 ggattcaatcttaagaaactttattgccaaatgtttgaacgatctgcttcggatcctcta 300

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APPLICANT: Leemans, Jan
TITLE OF INVENTION: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...JUBESS:
STREET: BIRCH, STEWART, KOLASCH & BIRCH
STREET: BILD Gatehouse Road, Suite 500 East
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 2046
MPUTER: 2046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tgttgataaccggtaccatggtagc 3374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/08351413
Patent No. 5750867
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-351-413-17
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complement (18..401)
ORNATION: /label- 3'nos
FORMATION: /note- "3' regulatory sequence containing the
FORMATION: polyademylation site derived from Agrobacterium
The synthase gene"
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OTHER INFORMATION: /label= 3583
OTHER INFORMATION: /note= "'3583" promoter sequence derived from OTHER INFORMATION: cauliflower mosaic virus isolate Cabbb-JI"
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RMATION: /label- barstar
RMATION: /note- "coding region of the barstar gene of
RMATION: Bacillus amyloliquefaciens"
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RAMITON: /label- PZM13
RMATION: /note= "promoter region of the Zm13 gene of RMATION: mays"
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RMATION: /label= pract
RMATION: /note= "promoter region of the TA29 gene of
RMATION: Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (402..737)
RMATION: /label- barnase
RMATION: /note= "coding region of the barnase gene
RMATION: Bacillus amyloliquefaciens"
YSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: ECORI-HindIII fragment of plasmid pTS218
                                                                                                                                                                                                                                                                         NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
TELEXX: 7,033 205-8050
                                                                                                 CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-UN-1992
REICR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: complement (1945..2281)
OTHER INFORMATION: /label= 3'nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 24845
INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERIFICS:
LENGTH: 4008 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
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FEATURE:
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LOCATION: complemen
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COTHER INFORMATION:
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FRAURE:
NAME/KEY:
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OTHER INFORMATION:
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FEATURE:
NAME/KEY:
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                                                                                    FILING DATE
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OTHER INFORMATION: /label= 3, nos
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA nopaline synthase gene"
3286 tttgtaatgtaattatcaggtagcttatgatatgtctgaagataatccgcaacccgtca
                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: B110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Viginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: EcoRI-HindIII fragment of plasmid pTS218
                                                                                                                                                            3346 aacgtgttgataaccggtaccatggtagc 3374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
FILING DATE: APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                 Sequence 17, Application US/09025583 Patent No. 5977433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 1.2
TELEX: 248345
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4808 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 21,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Svensson, Leonard R. REGISTRATION NUMBER: 30,33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Williams, Mark
                                                                                                                                                                                                                                                                                                                                                                                          Leemans, Jan
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US-09-025-583-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cttttgcccgggagtttgccttccctgtttgagaagatgtctccgccgatgcttttcccc 3225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 2333..2356
OTHER INFORMATION: /label= BXOL2
OTHER INFORMATION: /note= "region corresponding to oligonucleotide OTHER INFORMATION: BXOL2"
                                                                                                                                                                                                                                                                                                                          complement (2538..2586)
RMATION: /label= TA29SBXOL2
RMATION: /note= "region complementary to oligonucleotide RMATION: TA29SBXOL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TGCGGGACTCTAATCATAAAACCCATCTCATAAATAACGTCATGCATTACATGTTAATT 180
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              OTHER INFORMATION: /label- bar
OTHER INFORMATION: /note- "coding region of the phosphinothricin
OTHER INFORMATION: acetyltransferase gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: complement (2800..2823)
COTHER INFORMATION: /label- PTA290L5
OTHER INFORMATION: /note- "region complementary to part
CTHER INFORMATION: oligonucleotide PTA290L5"
US-08-351-413-17
                                                                                                                                        /label= 3'nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 99.3
Matches 744; Conservative
                                                                                         NAME/KEY: - LOCATION: 4485..4763
OTHER INFORMATION: /
                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION: complement
COTHER INFORMATION: /
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OTHER INFORMATION: /label= BXOL2

OTHER INFORMATION: /note= "region corresponding to oligonucleotide OTHER INFORMATION: BXOL2"

OTHER INFORMATION: BXOL2"

NAME/KET: - LCCATION: /note= "region complementary to oligonucleotide OTHER INFORMATION: /note= "region complementary to oligonucleotide FEATURE:

NAME/KET: - LCCATION: /note= "region complementary to oligonucleotide FEATURE:

LCCATION: /label= PTA2950L5

OTHER INFORMATION: /label= PTA290L5

OTHER INFORMATION: /label= PTA290L5

OTHER INFORMATION: /note= "region complementary to part of OTHER INFORMATION: /label= PTA290L5

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LOCATION: 3100.3932

OTHER INFORMATION: /label= 3553 .
OTHER INFORMATION: /note= "3553 promoter sequence derived from other information: cauliflower mosaic virus isolate Cabbb-JI"

NAME/KEY: -
LOCATION: 333.4.484

OTHER INFORMATION: /label= bar
OTHER INFORMATION: /note= "coding region of the phosphinothricin FEATURE:
NAME/KEY: -
LOCATION: 4465.4763
OTHER INFORMATION: /label= 3'nos
FEATURE:
NAME/KEY: -
LOCATION: /label= 3'nos
FEATURE:
NAME/KEY: -
LOCATION: /label= 3'nos
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                      complement (402..737)
RMATION: /label- barnase
RMATION: /note- "coding region of the barnase gene
RMATION: Bacillus amyloliquefaciens"
                                                                                                                                                                                                                                                                                                                                        LOCATION: complement (2282..2554)
OTHER INFORMATION: /label= barstar
OTHER INFORMATION: /label= barstar
OTHER INFORMATION: /label= barstar
OTHER INFORMATION: Bacillus amyloliquefaciens"
NAME/KEY:
LOCATION: complement (2555..3099)
OTHER INFORMATION: /label= PTA29
OTHER INFORMATION: /note= "promoter region of the TA29 gene of the INFORMATION: Nicotiana tabacum"
                                                                                                                                                                                                 gene
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                                                                                                                                                                                            region
NAME/KEY:

LOCATION: complement (402..737)

LOCATION: complement (402..737)

OTHER INFORMATION: /Label= barnase
OTHER INFORMATION: /Label= coding regio
OTHER INFORMATION: Bacillus amyloliquef
FRATURE:
LOCATION: complement (738..1944)
OTHER INFORMATION: /Label= PZM13
OTHER INFORMATION: /Label= PZM3
OTHER INFORMATION: /Label= PZM3
OTHER INFORMATION: /Label= Location
FRATURE:
NAME/KEY:
LOCATION: complement (1945..2281)
OTHER INFORMATION: /Label= 3'nos
                                                                                                                                                                                                                                                                                                                             NAME/KEY: -
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      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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JOURNAL Unpublished (1997) COMMENT Contact: Ecker J. Arabidopsis Thaliana Genome Center University of Pennsylvania Dept. of Biology, University of Pennsylvania, Philadelphia, PA	19104 Tel: 215-898-9384 Fax: 215-898-8780 Email: jecker@atgenome.bio.upenn.edu Seq primer: T Class: BAC ends. Location/Qualifiers 1. 796 /organism="Arabidopsis thaliana" /strain="Tolumbia" /db.xref="taxon:3702" /clone="Toksty" /clone="Toksty" /sex="hermaphrodite" /note="Yecktor: BeloBACII; Site_1: HindIII; Site_2: HindIII /sex="hermaphrodite" /note="Yecktor: BeloBACII; Site_1: HindIII; Site_2: HindIII /sex="hermaphrodite" /note="Yecktor: BeloBACII; Site_1: HindIII; Site_2: HindIII /sex="hermaphrodite" /note="Yecktor: BeloBACII; Site_1: HindIII]	Ouery Match Query Match Query Match Query Match Best Local Similarity Be 6%; Score 565.2; DB 226; Length 796; Batches 657; Conservative 0; Mismatches 99; Indels 3; Gaps 3; Oy 964 caagctttggagtgatcggagggtctaggatacatgagatctac 1023 I	1144 aagataattocatgaatcttatcgttatctatgagtgaattgtgtgatggtgggggggg	3/5 1384 435 1444 495 1504 554 514
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1 149 c 140 g 272 t 2 others
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Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and
Contact: Ecker J.
Arabidopsis Thallana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
Tel: 215-898-9384
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T24K7-T7.1 TAMU Arabidopsis thaliana genomic clone T24K7, DNA
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Pred. No. 5.1e-100;
0; Mismatches 84; Indels 11:
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                                                          thaliana"
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Best Local Similarity 87.8
Matches 685; Conservative
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Class: BAC ends.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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282 GCTCATTTTACTTGCCTGGTGGACTTGGCCCTTTCCTTATGGGGGAATTTATATTTTACTT 341
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T26K17-T7 TAMU Arabidopsis thaliana genomic clone T26K17, DNA
                                Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia,
19104
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Fax: 215-898-8780
Fmail: jecker@atgenome.bio.upenn.edu
Seg primer: T7
Class: BAC ends.
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/organism="Arabidopsis
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Contact: Ecker J.
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/note="Vector: BeloBACII; Site_1: HindIII; Site_2: HindIII; Produced by Rod Wing" 3 others
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
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AL061936.1 GI:4940214
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
Genoscope.
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Pred. No. 5.3e-52;
0; Mismatches 67; Indels
                                                                                              thaliana"
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Email: jecker@atgenome.bio.upenn.edu
Seg primer: T7
Class: BAC ends.
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                                                               Location/Qualifiers
                                                                                                            /strain="Columbia
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Best Local Similarity 84.6%;
Matches 384; Conservative
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis Thaliana Genome Center
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            - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila Malanogaster BAC ilbrary was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial isogenic strain y2; cn bw spy. the same strain used for the BDGP's and the EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library of filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
                                  carried out as part of a Genome Project (BDGP).
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Tetraodon nigroviridis DNA sequence
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clc
215D15 of library G from Tetraodon nigroviridis, genomic survey
   Tetraodontidae, Tetraodon.

1 (bases 1 to 625)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.
Saurin, W. and Weissenbach, J.
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Pred. No. 3e-08;
5; Mismatches 231; Indels 0;
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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Direct Submission
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr )
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
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Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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L Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRT cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr - Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Dirosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pland BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://pacpec.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
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1479 atgaaaataagaactttcaaaaaacagaactatgtttaatgtgtaaagattagtcgcaca 1538
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Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
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FEATURES

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The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and Aaron Mammoser in Patera de Jons's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial isoganic strain v2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
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/db_xref="Laxon:7227"
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PW 131 JAVOU DAYNE LEARNING (E. MEALL ) SEQUELY SHOULD SHOW THE PROPERTY OF A COLLABORATION Of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila Aaron Mammoser BAC library was prepared by Kazuctoy Ososegawa and Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial isogenic strain y2; cn bw sp, the same strain used for the BDGP is and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
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80; Conservative 300; Mismatches 294; Indels
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/db_xref="Laxon:7227"
/clone_lib="RPCI-98"
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/tissue_type="seedling green leaf"
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
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                                                                                                                                                                                                                                                                                                                     tacatcacttccctatcggattgaatgttttacttgtaccttttccgttgcaatgatatt 1856
                                                                                                                                                      gatagtatgtttgtgaaaactaatagggttaacaatcgaagtcatggaatatggatttgg 1916
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                                     737 TACTYHYHHHHYHWAYHTTWYAWAHAMWMHHAHYAAAAAAWAAWATTHHYHHTTHYMHH 796
                gaaaactatacacaaaacaagtcagataaatctctttctgggcctgtcttcccaacctcc
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65, Last updated, Version 1)
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Email: rwing@clemson.edu
Seg primer: ArryAAACCTCACTAAAAGGG
High quality sequence start: 39
High quality sequence stop: 1197.
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Clemson University
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EWRX cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr )

Determination of this BAC-end sequence was carried out as part of & Collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Prosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Prosophila melanogaster BAC library (Dros. E-celiano University Alain Billaud at CEPH (Centre Indiana Provided by a MRC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIGLATY (DIOS BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genewieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37L10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                          2118 mattogatoagtgtggmattgtmommanatttgggmatotactatatatatataatgottt 2177
                                                                                                                     2178 acaacacttggatttttttttggaggctggaatttttaatctacatatttgttttggcca 2237
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Best Local Similarity 37.4%; Pred. No. 1.6e-07;
Matches 226; Conservative 75; Mismatches 303; Indels 0.
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Plasmid Drosophila melanogaster
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AL Submission

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Direct Submission

Submitted (102-UNI-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley prosphila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the
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                                         ttcatgaataaaaatgggaaatttttgaatttgtactgctaaatgcataagattaggtga
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                                                                                                                          aactgtggaatatatttttttttcatttaaaagcaaaatttgccttttactagaattata
                                                                                                                                                               1447 aatatagaaaaatatataacattcaaataaaaatgaaaataagaactttcaaaaaacaga
                                                                                                                                                                                                                                                1507 actatgittaaigigtaaagattagicgcacaicaagicaictgitacaataigitacaa
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/db_xref="taxon:727"
/clone_lib="RPCI-98"
/clone="BACR14H09"
/note="end : TET3"
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Direct Submissions

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers

Location/Qualifiers
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebl.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton pBeloBACII.
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                     Drosophila melanogaster genome survey sequence T7 end of BAC BACNISM24 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL106396.1 GI:5621701
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Musconorpha; Ephydroidea; Drosophilidae; Drosophila.
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/plasmid="pBeloBAC11"
/db_xref="taxon:722"
/clone_lbb"DrosBAC"
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tive 65; Mismatches 217;
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1 (bases I to 529)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full.length cDNA libraries and normalization

Unpublished (2001)
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Homo sapiens cDNA clone CLOBB002ZE09
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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14.4%; Pred. No. 7.3e-07;
Ive 28; Mismatches 239;
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